

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:29:28 ; Search time 0.001 Seconds
(without alignments)
241.650 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgcgcg.....tccttcacgtttctttccccc 1611

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 segs, 75 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : rst2.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28	1.7	28	1	H22321
C 2	25	1.6	25	1	AA469268
C 3	19.4	1.2	22	1	AA921198

ALIGNMENTS

RESULT 1
H22321/c
LOCUS H22321 28 bp mRNA linear EST 06-JUL-1995
DEFINITION Y136d09.r1 Soares breast 3NBHSt Homo sapiens cDNA clone IMAGE:160337 5' similar to SP:RS5_RAT P24050 40S RIBOSOMAL PROTEIN ;, mRNA sequence.
ACCESSION H22321
VERSION H22321.1 GI:891016
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 28)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 798
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 798 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1. 28
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/mol_type="mRNA"
/db_xref="GDB:574362"
/db_xref="taxon:9606"
/clone="IMAGE:160337"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NBHSt"
/note="Organ: breast; Vector: p77T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p77T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES
source

Query Match 1.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 CGCTGGTGTCTGTCTCTCCACTCGGTC 46
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DB 28 CGCTGGTGTCTGTCTCTCCACTCGGTC 1

RESULT 2

AA469268/c
LOCUS AA469268 25 bp mRNA linear EST 15-AUG-1997
DEFINITION nc68a03.s1 NCI_CGAP Prl Homo sapiens cDNA clone IMAGE:771724 similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. ;, mRNA sequence.
ACCESSION AA469268
VERSION AA469268.1 GI:2195802
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 1.
Location/Qualifiers
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:771724"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr1"
/note="Vector: pAMP10; Site 1: Not1; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CGCTGGTGTGCTGTCTCCCACTCG 43
|||||
Db 25 CGCTGGTGTGCTGTCTCCCACTCG 1

RESULT 3
AA921198
LOCUS
DEFINITION
vz27f12.r1 Soares_thymus_2NBMT Mus musculus cDNA clone
IMAGE:1327727 5' similar to SW:HIDA_MOUSE C09106 HISTONE
DEACETYLASE HD1. [3] SW:HIDA_MOUSE TR:Q92534 ; mRNA sequence.
AA921198
AA921198.1 GI:3067977
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 22)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:687271
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

FEATURES
source
/clone="IMAGE:1327727"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares thymus 2NBMT"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 1.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1098 TACAATGACTACTTTGAATAC 1118
|||||
Db 2 TACAACGACTACTTTGAATAC 22

Search completed: June 24, 2004, 10:29:28
Job time : 0.001 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:25:52 ; Search time 1 Seconds
(without alignments)
3.783 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgccg.....tcctcacgtttctttcccc 1611

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 73 seqs, 1174 residues

Total number of hits satisfying chosen parameters: 146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 73 summaries

Database : rnpn2.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21.8	1.4	25	1	US-10-859-198-165232
C 2	19.4	1.2	21	1	PCT-US04-00035-43855
C 3	17.8	1.1	21	1	PCT-US04-00035-43856
C 4	17.4	1.1	19	1	US-10-708-951-20883
C 5	17.4	1.1	19	1	US-10-708-951-45576
C 6	16.8	1.0	21	1	PCT-US04-00035-12071
C 7	16.8	1.0	21	1	PCT-US04-00035-28225
C 8	16.8	1.0	21	1	PCT-US04-00035-28228
C 9	16.8	1.0	21	1	US-10-847-918-12383
C 10	16.6	1.0	17	1	PCT-US02-38147A-198
C 11	16.4	1.0	20	1	US-10-057-550C-27
C 12	14.4	0.9	16	1	US-10-138-674B-5827
C 13	14.4	0.9	17	1	PCT-US03-41025-86
C 14	14.4	0.9	17	1	US-10-138-674B-4754
C 15	14.4	0.9	17	1	US-10-138-674B-7632
C 16	13.8	0.9	17	1	US-10-364-412A-3345
C 17	13.8	0.9	17	1	US-10-364-412A-3942
C 18	13.8	0.9	17	1	US-10-364-412A-5702
C 19	13.8	0.9	17	1	US-10-364-412A-5749
C 20	13.8	0.9	17	1	US-10-138-674B-947
C 21	13.8	0.9	17	1	US-10-138-674B-2635
C 22	13.8	0.9	17	1	US-10-138-674B-4755
C 23	13.8	0.9	17	1	US-10-138-674B-4756
C 24	13.8	0.9	17	1	US-10-138-674B-4757
C 25	13.8	0.9	17	1	US-10-138-674B-4758
C 26	13.8	0.9	17	1	US-10-138-674B-5394
C 27	13.8	0.9	17	1	US-10-138-674B-7633
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C 29	13.4	0.8	15	1	US-10-834-967-3951
C 30	13.4	0.8	15	1	US-10-364-412A-5002
C 31	13.4	0.8	15	1	US-10-364-412A-5050
C 32	13.4	0.8	16	1	US-10-834-967-3378
C 33	13	0.8	13	1	US-10-257-017B-145445

C 34	13	0.8	13	1	US-10-257-017B-145446	Sequence 145446,
C 35	13	0.8	13	1	US-10-257-017B-151965	Sequence 151965,
C 36	13	0.8	13	1	US-10-257-017B-151966	Sequence 151966,
C 37	13	0.8	13	1	US-10-708-951-20910	Sequence 20910, A
C 38	13	0.8	13	1	US-10-708-951-46339	Sequence 46339, A
C 39	12.8	0.8	16	1	US-10-708-951-21093	Sequence 21093, A
C 40	12.8	0.8	16	1	US-10-708-951-46804	Sequence 46804, A
C 41	12.8	0.8	16	1	US-10-364-412A-5277	Sequence 5277, Ap
C 42	12.8	0.8	16	1	US-10-364-412A-7505	Sequence 7505, Ap
C 43	12.8	0.8	16	1	US-10-364-412A-7832	Sequence 7832, Ap
C 44	12.8	0.8	16	1	US-10-364-412A-7834	Sequence 7834, Ap
C 45	12.8	0.8	16	1	US-10-364-412A-8999	Sequence 8999, Ap
C 46	12.8	0.8	16	1	US-10-138-674B-5988	Sequence 5988, Ap
C 47	12.6	0.8	13	1	US-10-257-017B-41893	Sequence 41893, A
C 48	12.6	0.8	13	1	US-10-257-017B-41894	Sequence 41894, A
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C 51	12.6	0.8	13	1	US-10-257-017B-188275	Sequence 188275,
C 52	12.6	0.8	13	1	US-10-257-017B-188276	Sequence 188276,
C 53	12.4	0.8	14	1	US-10-708-951-31160	Sequence 31160, A
C 54	12.4	0.8	14	1	US-10-708-951-43411	Sequence 43411, A
C 55	12.4	0.8	15	1	US-10-796-280-67926	Sequence 67926, A
C 56	12.4	0.8	15	1	US-10-708-951-20715	Sequence 20715, A
C 57	12.4	0.8	15	1	US-10-708-951-22787	Sequence 22787, A
C 58	12.4	0.8	15	1	US-10-708-951-40578	Sequence 40578, A
C 59	12.4	0.8	15	1	US-10-708-951-45190	Sequence 45190, A
C 60	12.4	0.8	15	1	US-10-834-967-1542	Sequence 1542, Ap
C 61	12.4	0.8	15	1	US-10-834-967-4433	Sequence 4433, Ap
C 62	12.4	0.8	15	1	US-10-364-412A-1121	Sequence 1121, Ap
C 63	12.4	0.8	15	1	US-10-364-412A-1178	Sequence 1178, Ap
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C 65	12.4	0.8	15	1	US-10-364-412A-3852	Sequence 3852, Ap
C 66	12.4	0.8	15	1	US-10-364-412A-4291	Sequence 4291, Ap
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C 68	12.4	0.8	15	1	US-10-364-412A-5773	Sequence 5773, Ap
C 69	12.4	0.8	15	1	US-10-364-412A-5828	Sequence 5828, Ap
C 70	12.4	0.8	15	1	US-10-364-412A-6612	Sequence 6612, Ap
C 71	12.4	0.8	15	1	US-10-364-412A-6645	Sequence 6645, Ap
C 72	12.4	0.8	15	1	US-10-364-412A-8313	Sequence 8313, Ap
C 73	12.4	0.8	15	1	US-10-364-412A-8326	Sequence 8326, Ap

ALIGNMENTS

RESULT 1
US-10-859-198-165232/c
; Sequence 165232, Application US/10859198
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; APPLICANT: Murphy, Ellen
; APPLICANT: Whitley, Maryann
; TITLE OF INVENTION: Nucleic Acid Arrays for Detecting Multiple Strains of a Non-Viral
; FILE REFERENCE: 031896-014000 (AM101085)
; CURRENT APPLICATION NUMBER: US/10/859,198
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/475,871
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 282011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe sequence
US-10-859-198-165232

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 334 TCTTGGCTCCATCCGTCAGATAA 358

Db 25 TCTTGGCTACATCCGGTACAGATAA 1
RESULT 2
PCT-US04-00035-43855/c
; Sequence 43855, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43855
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-00035-43855
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 131 CCGGAGGAGAAAGTCTGTTACTA 151
Db 21 CCGGAGGAGAAAGTCGGTTACTA 1
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PCT-US04-00035-43856/c
; Sequence 43856, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43856
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
PCT-US04-00035-43856
Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 129 ACCCGGAGGAAAGTCTGTTAC 149
Db 21 AACCGGAGGAAAGTCGGTTAC 1
RESULT 4
US-10-708-951-20883/c
; Sequence 20883, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20883
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20883
Query Match 1.1%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 465 GCAAGTGTCTGTGAAACTTA 483
Db 19 GTAAGTGTGTGAAACTTA 1
RESULT 5
US-10-708-951-45576/c
; Sequence 45576, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45576
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-45576
Query Match 1.1%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 465 GCAAGTGTCTGTGAAACTTA 483
Db 19 GTAAGTGTGTGAAACTTA 1
RESULT 6
PCT-US04-00035-12071
; Sequence 12071, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12071
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
PCT-US04-00035-12071
Query Match 1.0%; Score 16.8; DB 1; Length 21;

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US-10-847-918-12383/c
; Sequence 12383, Application US/10847918
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12383
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-12383
Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 957 AAGTGTGTGGAATTGTGCAA 976
| | | | | | | | | | | | | | | | | | | |
DB 21 AAGTGTGTGCAATGTGCAA 2
| | | | | | | | | | | | | | | | | | | |
RESULT 10
PCT-US02-38147A-198/c
; Sequence 198, Application PC/TUS0238147A
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: 66797-164 (IX 5532)
; CURRENT APPLICATION NUMBER: PCT/US02/38147A
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147A-198
Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1453 AAAAGAGAGAAAGACCCA 1469
| | | | | | | | | | | | | | | | | | | |
DB 17 AAAAGAGAGAAAGAYCCA 1
| | | | | | | | | | | | | | | | | | | |
RESULT 11
US-10-057-550C-27/c
; Sequence 27, Application US/10057550C
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
US-10-847-918-12383/c
; Sequence 12383, Application US/10847918
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12383
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-12383
Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 957 AAGTGTGTGGAATTGTGCAA 976
| | | | | | | | | | | | | | | | | | | |
DB 21 AAGTGTGTGCAATGTGCAA 2
| | | | | | | | | | | | | | | | | | | |
RESULT 10
PCT-US02-38147A-198/c
; Sequence 198, Application PC/TUS0238147A
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: 66797-164 (IX 5532)
; CURRENT APPLICATION NUMBER: PCT/US02/38147A
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147A-198
Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1453 AAAAGAGAGAAAGACCCA 1469
| | | | | | | | | | | | | | | | | | | |
DB 17 AAAAGAGAGAAAGAYCCA 1
| | | | | | | | | | | | | | | | | | | |
RESULT 11
US-10-057-550C-27/c
; Sequence 27, Application US/10057550C
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
US-10-847-918-12383/c
; Sequence 12383, Application US/10847918
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12383
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-12383
Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 957 AAGTGTGTGGAATTGTGCAA 976
| | | | | | | | | | | | | | | | | | | |
DB 21 AAGTGTGTGCAATGTGCAA 2
| | | | | | | | | | | | | | | | | | | |
RESULT 10
PCT-US02-38147A-198/c
; Sequence 198, Application PC/TUS0238147A
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: 66797-164 (IX 5532)
; CURRENT APPLICATION NUMBER: PCT/US02/38147A
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147A-198
Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1453 AAAAGAGAGAAAGACCCA 1469
| | | | | | | | | | | | | | | | | | | |
DB 17 AAAAGAGAGAAAGAYCCA 1
| | | | | | | | | | | | | | | | | | | |
RESULT 11
US-10-057-550C-27/c
; Sequence 27, Application US/10057550C
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression

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; FILE REFERENCE: ISPH-0625
; CURRENT APPLICATION NUMBER: US/10/057,550C
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-057-550C-27

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 12

US-10-138-674B-5827
; Sequence 5827, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

RESULT 13

PCT-US03-41025-86
; Sequence 86, Application PC/TUS0341025
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Langdown, Maria L.
; APPLICANT: Nelson, Matthew Roberts
; APPLICANT: Reneland, Rikard Henry
; APPLICANT: Kammerer, Stefan M.
; APPLICANT: Braun, Andreas

; APPLICANT: Dennissenko, Mikhail F.
; APPLICANT: Atienza, Josephine M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF TYPE II
; TITLE OF INVENTION: DIABETES AND TREATMENTS THEREOF
; FILE REFERENCE: 524592007340
; CURRENT APPLICATION NUMBER: PCT/US03/41025
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,431
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/498,970
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/498,100
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/477,437
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US03-41025-86

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1218 CTTAGAATGCTGCCGC 1233
Db 2 CTTAGAATGCTGCCTC 17

RESULT 14

US-10-138-674B-4754
; Sequence 4754, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions f
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4754

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 18;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

RESULT 15

US-10-138-674B-7632
; Sequence 7632, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan

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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-7632

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 18;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      516 GCTGGGGGCGCTGCACC 531
Db      2 GCUGGGAGCCUGCACC 17

RESULT 16
US-10-364-412A-3345
; Sequence 3345, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3345
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (696917)...(696933)
; OTHER INFORMATION: Chromosome = 7 Strand = positive ConnectronObjectNumber = 6259
US-10-364-412A-3345

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1293 GATGAGGACGAGACGA 1309
Db      1 GATGATGACGATGACGA 17

RESULT 17
US-10-364-412A-3942/c
; Sequence 3942, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3942
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (347222)...(347238)
; OTHER INFORMATION: Chromosome =14 Strand = negative ConnectronObjectNumber = 12372
US-10-364-412A-3942

Query Match      0.9%; Score 13.8; DB 1; Length 17;
```

```
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1293 GATGAGGACGAGACGA 1309
Db      17 GATGATGACGATGACGA 1

RESULT 18
US-10-364-412A-5702/c
; Sequence 5702, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5702
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (394472)...(394488)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 580
US-10-364-412A-5702

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1293 GATGAGGACGAGACGA 1309
Db      17 GATGACGACGACGACGA 1

RESULT 19
US-10-364-412A-5749/c
; Sequence 5749, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (576156)...(576172)
; OTHER INFORMATION: Chromosome =11 Strand = positive ConnectronObjectNumber = 939
US-10-364-412A-5749

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1293 GATGAGGACGAGACGA 1309
Db      17 GATGACGACGACGACGA 1

RESULT 20
US-10-138-674B-947
; Sequence 947, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
```


APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 947
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-947

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 23;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAAACTT 482
Db 1 CAACUGCUUUGAAACUU 17

RESULT 21

US-10-138-674B-2635/c
Sequence 2635, Application US/10138674B
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2635
LENGTH: 17
TYPE: RNA
ORGANISM: Mus musculus
US-10-138-674B-2635

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGTC 34
Db 17 CTGCTGGTGTGCTGTC 1

RESULT 22

US-10-138-674B-4755
Sequence 4755, Application US/10138674B
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4755
LENGTH: 17

TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-4755

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 23;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCTGCACCATG 534
Db 1 UGGAGCCUGACCAAG 17

RESULT 23

US-10-138-674B-4756
Sequence 4756, Application US/10138674B
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4756
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-4756

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCTGCACCATGCAA 537
Db 1 GAGCCUGACCAAGCAA 17

RESULT 24

US-10-138-674B-4757
Sequence 4757, Application US/10138674B
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4757
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-4757

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAAG 539
Db 1 GCCUGACCAAGCAAG 17

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-7633

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 519 GGGGGCCTGCACCATGC 535
Db 1 GGGAGCCUGCACCACG 17

RESULT 28
US-10-834-967-771
; Sequence 771, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connection Sequences for the Archaeoglobus fulgidus DSM 4304,
; TITLE OF INVENTION: complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 771
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (281999)...(282013)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = pos CtronObjNum = 771
US-10-834-967-771

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1381 AAGAGGAGGAGAGG 1395
Db 1 AAGAGCAGGAGAGG 15

RESULT 29
US-10-834-967-3951
; Sequence 3951, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connection Sequences for the Archaeoglobus fulgidus DSM 4304,
; TITLE OF INVENTION: complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 3951
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglcbus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (1581557)...(1581571)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = pos CtronObjNum = 3951
US-10-834-967-3951

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4758
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4758

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAGA 540
Db 1 CCUGCACCACCAAGGA 17

RESULT 26
US-10-138-674B-5394/c
; Sequence 5394, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5394
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-5394

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGGTGGAGGACTGTCC 412
Db 17 GGTGGAGAGGAGTGTCC 1

RESULT 27
US-10-138-674B-7633
; Sequence 7633, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```
Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1381 AAGAGGAGGGAGAGG 1395
Db 1 AAGAGCAGGGAGAGG 15

RESULT 30
US-10-364-412A-5002
; Sequence 5002, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5002
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (24168)...(24182)
; OTHER INFORMATION: Chromosome = 6 Strand = positive ConnectronObjectNumber = 5100
US-10-364-412A-5002

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1292 CGATGAGGACGAAGA 1306
Db 1 CGATGAGGATGAAGA 15

RESULT 31
US-10-364-412A-5050
; Sequence 5050, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5050
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (589372)...(589386)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 6170
US-10-364-412A-5050

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1292 CGATGAGGACGAAGA 1306
Db 1 CGATGAGGATGAAGA 15

RESULT 32
US-10-834-967-3378/c
; Sequence 3378, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connectron Sequences for the Archaeoglobus fulgidus DSM 4304,
```

```
; TITLE OF INVENTION: complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 3378
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (1349931)...(1349946)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = neg CtronObjNum = 3378
US-10-834-967-3378
```

```
Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1381 AAGAGGAGGGAGAGG 1395
Db 16 AAGAGGAGGAAGAGG 2
```

```
RESULT 33
US-10-257-017B-145445/c
; Sequence 145445, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosir
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145445
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036625
US-10-257-017B-145445
```

```
Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 249 CTCTACCGAAAA 261
Db 13 CTCTACCGAAAA 1
```

```
RESULT 34
US-10-257-017B-145446
; Sequence 145446, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosir
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145446
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036625
US-10-257-017B-14546

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTCTACCGAAAAA 261
Db 1 CTCTACCGAAAAA 13

RESULT 35
US-10-257-017B-151965/c
; Sequence 151965, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 151965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038398
US-10-257-017B-151965

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAA 1427
Db 13 CAACTTCAAAAAA 1

RESULT 36
US-10-257-017B-151966
; Sequence 151966, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 151966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038398
US-10-257-017B-151966

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1415 CAACTTCAAAAAA 1427
Db 1 CAACTTCAAAAAA 13

RESULT 37
US-10-708-951-20910
; Sequence 20910, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20910
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20910

Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 327 ATTAATTCCTTGC 339
Db 3 AUUAAAUUCUUGC 15

RESULT 38
US-10-708-951-46339
; Sequence 46339, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46339
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-46339

Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 327 ATTAATTCCTTGC 339
Db 3 AUUAAAUUCUUGC 15

RESULT 39
US-10-708-951-21093/c
; Sequence 21093, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21093
```

; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-21093

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 463 TGGCAAGTGCTGTGAA 478
Db 16 TTGTAAGTGCTGTGAA 1

RESULT 40
US-10-708-951-46804/c
; Sequence 46804, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46804
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-46804

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 463 TGGCAAGTGCTGTGAA 478
Db 16 TTGTAAGTGCTGTGAA 1

RESULT 41
US-10-364-412A-5277
; Sequence 5277, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5277
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (235019)...(235035)
; OTHER INFORMATION: Chromosome = 6 Strand = positive ConnectronObjectNumber = 5427
US-10-364-412A-5277

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGACGACGA 1309
Db 1 ATGACGACGACGACGA 16

RESULT 42
US-10-364-412A-7505
; Sequence 7505, Application US/10364412A

; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7505
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (768662)...(768678)
; OTHER INFORMATION: Chromosome =15 Strand = positive ConnectronObjectNumber = 1363
US-10-364-412A-7505

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGACGACGA 1309
Db 1 ATGACGACGACGACGA 16

RESULT 43
US-10-364-412A-7832/c
; Sequence 7832, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7832
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (999582)...(999597)
; OTHER INFORMATION: Chromosome =12 Strand = negative ConnectronObjectNumber = 107;
US-10-364-412A-7832

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGACGACGA 1309
Db 16 ATGATGACGACGACGA 1

RESULT 44
US-10-364-412A-7834/c
; Sequence 7834, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7834
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (1006862)...(1006877)
; OTHER INFORMATION: Chromosome =12 Strand = negative ConnectronObjectNumber = 107;
US-10-364-412A-7834


```
US-10-364-412A-7834
Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGAAGACGA 1309
    ||||| ||||| ||||| ||
Db 16 ATGATGACGAAGATGA 1

RESULT 45
US-10-364-412A-8999/c
; Sequence 8999, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 8999
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (768662)...(768678)
; OTHER INFORMATION: Chromosome =15 Strand = negative ConnectronObjectNumber = 13630
US-10-364-412A-8999

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGAAGACGA 1309
    ||||| ||||| ||||| ||
Db 16 ATGACGACGACGACGA 1

RESULT 46
US-10-138-674B-5988
; Sequence 5988, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5988
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-5988

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAAACT 481
    ||| :||: :|||:
Db 1 CAACUGCUUGAAACU 16

RESULT 47
US-10-257-017B-41893
```

```
; Sequence 41893, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41893
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012555
US-10-257-017B-41893

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1004 GGGAGGCGGTGGT 1016
    ||||| ||||| |||||
Db 1 GGGAGGCGGTGGY 13

RESULT 48
US-10-257-017B-41894/c
; Sequence 41894, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41894
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012555
US-10-257-017B-41894

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1004 GGGAGGCGGTGGT 1016
    ||||| ||||| |||||
Db 13 GGGAGGCGGTGGY 1

RESULT 49
US-10-257-017B-48345
; Sequence 48345, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```

; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 48345
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013790
US-10-257-017B-48345

```

```

Query Match      0.8%;   Score 12.6;   DB 1;   Length 13;
Best Local Similarity 92.3%;
Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Caps 0;

```

QY 853 TAATGGAGATGTT 865
|||||
Db 1 TAATGGAGATGTY 13

RESULT 50

```

US-10-257-017B-48346/c
; Sequence 48346, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 48346
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013790
US-10-257-017B-48346

```

Query Match	0.8%	Score 12.6;	DB 1;	Length 13;
Best Local Similarity	92.3%	Pred. No. 19;		
Matches 12; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 853 TAATGGAGATGTT 865
Db 13 TAATGGAGATGTY 1

RESULT 51

```

US-10-257-017B-188275
; Sequence 188275, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 188275
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00463575
US-10-257-017B-188275

Query Match 0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	256	GAAAAATCGAAAT	268
			:
Db	1	GAAAAATGGAAY	13

RESULT 52

US-10-257-017B-188276/c
; Sequence 188276, Application US/10257017B
; GENERAL INFORMATION:

/ APPLICANT: Alexander Olek
 / APPLICANT: Christian Piepenbrock
 / APPLICANT: Kurt Berlin
 / TITLE OF INVENTION: Detection of single nu
 / TITLE OF INVENTION: methylations
 / FILE REFERENCE: E01/1193/WO
 / CURRENT APPLICATION NUMBER: US/10/257,017B
 / CURRENT FILING DATE: 2002-10-07
 / PRIOR APPLICATION NUMBER: DE 10019173.8
 / PRIOR FILING DATE: 2000-04-07
 / NUMBER OF SEQ ID NOS: 382046
 / SEQ ID NO 188276

: LENGTH: 13

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; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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```

; OTHER INFORMATION: oligonucleotide for detection of SNP TSC0046357
US-10-257-017B-188276

```

Query Match 0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels

Qy 256 GAAAAATGGAAT 268
 |
Db 13 GAAAAATGGAAY 1

RESULT 53

US-10-708-951-31160
; Sequence 31160, Application US/10708951
: GENERAL INFORMATION:

APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 55034

FILE REFERENCE: 2004-04-02
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02

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; CURRENT LIBRARY NAME: 10010101
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31160

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: SEQ ID NO: 14
: LENGTH: 14

LENGTH: 13
TYPE: RNA
ORGANISM: Homo sapiens

US-10-708-951-31160

Query Match 0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 1; Indels

QY 269 CTATCGCCCTCACA 282
|:|:|:|:|:|:|:
Db , CTATCGCCCAUACA 14

RESULT 54
US-10-708-951-43411

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE.

; Sequence 43411, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43411
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-43411

Query Match 0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 269 CTATCGCCCTCACCA 282
Db 1 CUAUCGCCCAUCACA 14

RESULT 55
US-10-796-280-67926/c
; Sequence 67926, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67926
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-67926

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1268 GGACGCCATCCCTG 1281
Db 15 GGAAGCCATCCCTG 2

RESULT 56
US-10-708-951-20715
; Sequence 20715, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20715

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1559 AATGGACCTCTCCA 1572
Db 1 AAGGACCUCUCCA 14

RESULT 57
US-10-708-951-22787/c
; Sequence 22787, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22787
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-22787

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 640 TTCACCATGTTGAC 653
Db 15 TTCACCATGTTGAC 2

RESULT 58
US-10-708-951-40578
; Sequence 40578, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-40578

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1559 AATGGACCTCTCCA 1572
Db 1 AAGGACCUCUCCA 14

RESULT 59
US-10-708-951-45190/c
; Sequence 45190, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45190

```
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-951-45190

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      640 TTCACCATGGTGAC 653
Db      15 TTCACCATGTTGAC 2

RESULT 60
US-10-834-967-1542
; Sequence 1542, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connectron Sequences for the Archaeoglobus fulgidus DSM 4304,
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 1542
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (598308)...(598322)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = neg CtronObjNum = 1542
; US-10-834-967-1542

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      876 GCGGTGGTCTTACA 889
Db      2 GCGGTGGTGTACA 15

RESULT 61
US-10-834-967-4433
; Sequence 4433, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connectron Sequences for the Archaeoglobus fulgidus DSM 4304,
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 4433
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (1760153)...(1760167)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = pos CtronObjNum = 4433
; US-10-834-967-4433

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      876 GCGGTGGTCTTACA 889
Db      2 GCGGTGGTGTACA 15
```

```
RESULT 62
US-10-364-412A-1121/c
; Sequence 1121, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (714110)...(714124)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 13
; US-10-364-412A-1121

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1293 GATGAGACGAAGA 1306
Db      14 GATGAAGACGAAGA 1

RESULT 63
US-10-364-412A-1178/c
; Sequence 1178, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (720539)...(720553)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 63
; US-10-364-412A-1178

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1293 GATGAGACGAAGA 1306
Db      14 GATGAAGACGAAGA 1

RESULT 64
US-10-364-412A-3817/c
; Sequence 3817, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3817
; LENGTH: 15
; TYPE: DNA
```

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; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (1118706)...(1118720)
; OTHER INFORMATION: Chromosome = 4 Strand = negative ConnectronObjectNumber = 3584
US-10-364-412A-3817

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1446 GAGGATGAAAAAAGA 1459
      |||||
Db 14 GAGGATGAAGAAGA 1

RESULT 65
US-10-364-412A-3852/c
; Sequence 3852, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3852
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (404987)...(404901)
; OTHER INFORMATION: Chromosome =13 Strand = positive ConnectronObjectNumber = 11539
US-10-364-412A-3852

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1446 GAGGATGAAAAAAGA 1459
      |||||
Db 14 GAGGATGAAGAAGA 1

RESULT 66
US-10-364-412A-4291
; Sequence 4291, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 4291
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (274788)...(274802)
; OTHER INFORMATION: Chromosome = 5 Strand = positive ConnectronObjectNumber = 4481
US-10-364-412A-4291

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1444 CAGAGGATGAAAAA 1457
      |||||
Db 1 CAGAAGATGAAAAA 14
```

```

RESULT 67
US-10-364-412A-4292/c
; Sequence 4292, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 4292
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (274788)...(274802)
; OTHER INFORMATION: Chromosome = 5 Strand = negative ConnectronObjectNumber = 448
US-10-364-412A-4292

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1444 CAGAGGATGAAAAA 1457
      |||||
Db 15 CAGAAGATGAAAAA 2

RESULT 68
US-10-364-412A-5773/c
; Sequence 5773, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (720539)...(720553)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 630
US-10-364-412A-5773

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGACGAAGA 1306
      |||||
Db 14 GATGAAGACGAAGA 1

RESULT 69
US-10-364-412A-5828/c
; Sequence 5828, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
```


FEATURE:
LOCATION: (251903)...(251918)
OTHER INFORMATION: Chromosome =12 Strand = positive ConnexionObjectNumber = 9757
US-10-364-412A-5828

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGACGAAGA 1306
Db 14 GATGAGGACGAAGA 1

RESULT 70

US-10-364-412A-6612
Sequence 6612, Application US/10364412A

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/364,412A

CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 6612

LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.

FEATURE:
LOCATION: (155118)...(155132)
OTHER INFORMATION: Chromosome = 8 Strand = positive ConnexionObjectNumber = 7049
US-10-364-412A-6612

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1412 TTCCAACCTTCAAAA 1425
Db 1 TTCCAACCTTCAAAA 14

RESULT 71

US-10-364-412A-6645
Sequence 6645, Application US/10364412A

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/364,412A

CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 6645

LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.

FEATURE:
LOCATION: (868980)...(868994)
OTHER INFORMATION: Chromosome =16 Strand = negative ConnexionObjectNumber = 14895
US-10-364-412A-6645

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1412 TTCCAACCTTCAAAA 1425
Db 1 TTCCAACCTTCAAAA 14

RESULT 72

US-10-364-412A-8313
Sequence 8313, Application US/10364412A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/364,412A

CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 8313

LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.

FEATURE:
LOCATION: (58645)...(58659)
OTHER INFORMATION: Chromosome =13 Strand = negative ConnexionObjectNumber = 1091
US-10-364-412A-8313

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATATCGTC 581
Db 1 TCAATGATATCGAC 14

RESULT 73

US-10-364-412A-8326
Sequence 8326, Application US/10364412A

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/364,412A

CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 8326

LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.

FEATURE:
LOCATION: (195799)...(195813)
OTHER INFORMATION: Chromosome =13 Strand = positive ConnexionObjectNumber = 111
US-10-364-412A-8326

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATATCGTC 581
Db 1 TCAATGATATCGAC 14

Search completed: June 24, 2004, 10:25:54
Job time : 2 secs

107 14.8 0.9 18 1 US-09-923-246-23 Sequence 23, Appl
108 14.8 0.9 18 1 US-10-295-723-23 Sequence 23, Appl
109 14.8 0.9 18 1 US-10-243-072-22 Sequence 22, Appl
110 14.8 0.9 18 1 US-10-243-072-39 Sequence 39, Appl
111 14.8 0.9 18 1 US-10-414-186-22 Sequence 22, Appl
112 14.8 0.9 18 1 US-10-414-186-39 Sequence 39, Appl
113 14.8 0.9 18 1 US-10-659-684-23 Sequence 23, Appl
114 14.4 0.9 16 1 US-09-935-868-3 Sequence 3, Appl
115 14.4 0.9 16 1 US-10-287-035-3 Sequence 3, Appl
116 14.4 0.9 16 1 US-10-282-162-3 Sequence 3, Appl
117 14.4 0.9 16 1 US-10-138-674-5827 Sequence 5827, Ap
118 14.4 0.9 16 1 US-10-287-949A-5827 Sequence 5827, Ap
119 14.4 0.9 17 1 US-09-866-108-971 Sequence 971, App
120 14.4 0.9 17 1 US-09-866-108-972 Sequence 972, App
121 14.4 0.9 17 1 US-09-780-164-387 Sequence 387, App
122 14.4 0.9 17 1 US-09-780-164-966 Sequence 966, App
123 14.4 0.9 17 1 US-10-138-674-4754 Sequence 4754, Ap
124 14.4 0.9 17 1 US-10-138-674-7632 Sequence 7632, Ap
125 14.4 0.9 17 1 US-10-287-949A-4754 Sequence 4754, Ap
126 14.4 0.9 17 1 US-10-287-949A-7632 Sequence 7632, Ap
127 14.4 0.9 18 1 US-09-861-779-4 Sequence 4, Appl
128 14.4 0.9 18 1 US-10-636-716-4 Sequence 4, Appl
129 14.4 0.9 18 1 US-10-269-557-46 Sequence 46, Appl
130 14.4 0.9 18 1 US-10-367-438-165 Sequence 165, App
131 14.4 0.9 18 1 US-10-349-143-4102 Sequence 4102, Ap
132 14.4 0.9 18 1 US-10-349-143-9179 Sequence 9179, Ap
133 13.8 0.9 17 1 US-09-866-108-6562 Sequence 6562, Ap
134 13.8 0.9 17 1 US-09-866-108-7084 Sequence 7084, Ap
135 13.8 0.9 17 1 US-09-866-108-8667 Sequence 8667, Ap
136 13.8 0.9 17 1 US-09-866-108-8668 Sequence 8668, Ap
137 13.8 0.9 17 1 US-09-961-077-117 Sequence 117, App
138 13.8 0.9 17 1 US-09-784-674-66 Sequence 66, Appl
139 13.8 0.9 17 1 US-09-877-478-438 Sequence 438, App
140 13.8 0.9 17 1 US-09-848-754A-3128 Sequence 3128, Ap
141 13.8 0.9 17 1 US-09-827-395A-723 Sequence 723, App
142 13.8 0.9 17 1 US-09-740-332-1709 Sequence 1709, Ap
143 13.8 0.9 17 1 US-09-740-332-1724 Sequence 1724, Ap
144 13.8 0.9 17 1 US-09-740-332-2831 Sequence 2831, Ap
145 13.8 0.9 17 1 US-09-740-332-2846 Sequence 2846, Ap
146 13.8 0.9 17 1 US-09-740-332-4133 Sequence 4133, Ap
147 13.8 0.9 17 1 US-09-792-818-95 Sequence 95, Appl
148 13.8 0.9 17 1 US-09-817-879-1709 Sequence 1709, Ap
149 13.8 0.9 17 1 US-09-817-879-1724 Sequence 1724, Ap
150 13.8 0.9 17 1 US-09-817-879-2831 Sequence 2831, Ap
151 13.8 0.9 17 1 US-09-817-879-2846 Sequence 2846, Ap
152 13.8 0.9 17 1 US-09-817-879-4133 Sequence 4133, Ap
153 13.8 0.9 17 1 US-10-342-902-438 Sequence 438, App
154 13.8 0.9 17 1 US-09-949-298-2 Sequence 2, Appl
155 13.8 0.9 17 1 US-09-927-046-108 Sequence 108, App
156 13.8 0.9 17 1 US-10-430-882-723 Sequence 723, App
157 13.8 0.9 17 1 US-10-060-756A-588 Sequence 588, App
158 13.8 0.9 17 1 US-10-060-756A-589 Sequence 589, App
159 13.8 0.9 17 1 US-10-060-756A-590 Sequence 590, App
160 13.8 0.9 17 1 US-10-060-756A-591 Sequence 591, App
161 13.8 0.9 17 1 US-10-060-998-1329 Sequence 1329, Ap
162 13.8 0.9 17 1 US-10-163-552-559 Sequence 559, App
163 13.8 0.9 17 1 US-10-156-306-4432 Sequence 4432, Ap
164 13.8 0.9 17 1 US-10-156-306-4966 Sequence 4966, Ap
165 13.8 0.9 17 1 US-10-156-306-5928 Sequence 5928, Ap
166 13.8 0.9 17 1 US-10-156-306-6988 Sequence 6988, Ap
167 13.8 0.9 17 1 US-10-238-700-3037 Sequence 3037, Ap
168 13.8 0.9 17 1 US-10-238-700-3128 Sequence 3128, Ap
169 13.8 0.9 17 1 US-10-339-782-240 Sequence 240, App
170 13.8 0.9 17 1 US-10-297-068-971 Sequence 971, App
171 13.8 0.9 17 1 US-10-138-674-947 Sequence 947, App
172 13.8 0.9 17 1 US-10-138-674-2635 Sequence 2635, Ap
173 13.8 0.9 17 1 US-10-138-674-4755 Sequence 4755, Ap
174 13.8 0.9 17 1 US-10-138-674-4756 Sequence 4756, Ap
175 13.8 0.9 17 1 US-10-138-674-4757 Sequence 4757, Ap
176 13.8 0.9 17 1 US-10-138-674-4758 Sequence 4758, Ap
177 13.8 0.9 17 1 US-10-138-674-5394 Sequence 5394, Ap
178 13.8 0.9 17 1 US-10-138-674-7633 Sequence 7633, Ap
179 13.8 0.9 17 1 US-10-287-949A-947 Sequence 947, App

c 180 13.8 0.9 17 1 US-10-287-949A-2635 Sequence 2635, Ap
181 13.8 0.9 17 1 US-10-287-949A-4755 Sequence 4755, Ap
182 13.8 0.9 17 1 US-10-287-949A-4756 Sequence 4756, Ap
183 13.8 0.9 17 1 US-10-287-949A-4757 Sequence 4757, Ap
184 13.8 0.9 17 1 US-10-287-949A-4758 Sequence 4758, Ap
185 13.8 0.9 17 1 US-10-287-949A-5394 Sequence 5394, Ap
186 13.8 0.9 17 1 US-10-287-949A-7633 Sequence 7633, Ap
187 13.8 0.9 17 1 US-10-712-672-978 Sequence 978, App
188 13.8 0.9 17 1 US-10-712-672-2255 Sequence 2255, Ap
189 13.4 0.8 15 1 US-10-287-919-1912 Sequence 1912, Ap
190 13.4 0.8 15 1 US-10-287-919-1925 Sequence 1925, Ap
191 13.4 0.8 16 1 US-09-420-433-19 Sequence 19, Appl
192 13 0.8 15 1 US-09-945-505-18 Sequence 18, Appl
193 13 0.8 15 1 US-10-056-414-258 Sequence 258, App
194 13 0.8 15 1 US-10-043-875-250 Sequence 250, App
195 13 0.8 15 1 US-10-101-030B-48 Sequence 48, Appl
196 13 0.8 15 1 US-10-084-839-3505 Sequence 3505, Ap
197 13 0.8 16 1 US-10-084-839-3483 Sequence 3483, Ap
198 13 0.8 16 1 US-10-084-839-3501 Sequence 3501, Ap
199 13 0.8 16 1 US-10-277-216-330 Sequence 330, App
200 13 0.8 16 1 US-10-126-022-330 Sequence 330, App
201 12.8 0.8 16 1 US-08-591-486B-124 Sequence 124, App
202 12.8 0.8 16 1 US-09-739-928-11 Sequence 11, Appl
203 12.8 0.8 16 1 US-10-339-674-569 Sequence 569, App
204 12.8 0.8 16 1 US-10-059-888-22 Sequence 22, Appl
205 12.8 0.8 16 1 US-10-059-877-22 Sequence 22, Appl
206 12.8 0.8 16 1 US-10-065-133A-35 Sequence 35, Appl
207 12.8 0.8 16 1 US-10-434-811A-35 Sequence 35, Appl
208 12.8 0.8 16 1 US-10-138-674-5988 Sequence 5988, Ap
209 12.8 0.8 16 1 US-10-287-949A-5988 Sequence 5988, Ap

ALIGNMENTS

RESULT 1

US-09-563-728A-4/c
; Sequence 4, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-4

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTTGCTG 236
|||||
Db 26 GAATCCGCATGACTCATAATTTGCTG 1

RESULT 2

US-09-563-728A-13/c
; Sequence 13, Application US/09563728A
; Publication No. US20030078216A1

; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-13

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 3
US-10-145-493B-47/c
; Sequence 47, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-47

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 4
US-10-189-818B-39/c
; Sequence 39, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:

; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-189-818B-39

Query Match 1.6%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 8.5;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GTCAAGGAGGAGGCCAAGTTGGCTGAATG 1562
Db 30 GTCAAGGAGGAGGTCGACTTGGCTGAATG 1

RESULT 5
US-10-145-493B-90/c
; Sequence 90, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-90

Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACTCATAATTGCTG 1

RESULT 6
US-09-563-728A-2/c
; Sequence 2, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A

; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/132,287
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: oligonucleotide
 US-09-563-728A-2

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 8;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
 |||||
 Db 26 GAATCCGCATGACCCATAATTGCTG 1

RESULT 7
 US-09-563-728A-3/c
 ; Sequence 3, Application US/09563728A
 ; Publication No. US20030078216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLeod, Alan R
 ; APPLICANT: Li, Zoumei
 ; APPLICANT: Besterman, Jeffrey M
 ; TITLE OF INVENTION: Inhibition of Histone Deacetylase
 ; FILE REFERENCE: 106101.229
 ; CURRENT APPLICATION NUMBER: US/09/563,728A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/132,287
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: oligonucleotide
 US-09-563-728A-3

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 8;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
 |||||
 Db 26 GAATCCGCATGACTCATAACTGCTG 1

RESULT 8
 US-09-563-728A-11/c
 ; Sequence 11, Application US/09563728A
 ; Publication No. US20030078216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLeod, Alan R
 ; APPLICANT: Li, Zoumei
 ; APPLICANT: Besterman, Jeffrey M
 ; TITLE OF INVENTION: Inhibition of Histone Deacetylase
 ; FILE REFERENCE: 106101.229
 ; CURRENT APPLICATION NUMBER: US/09/563,728A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/132,287
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: 1-4 and 23-26 are modified
 ; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
 ; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
 ; OTHER INFORMATION: deoxyribonucleotides
 US-09-563-728A-11

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 8;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
 |||||
 Db 26 GAATCCGCATGACCCATAATTGCTG 1

RESULT 9
 US-09-563-728A-12/c
 ; Sequence 12, Application US/09563728A
 ; Publication No. US20030078216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLeod, Alan R
 ; APPLICANT: Li, Zoumei
 ; APPLICANT: Besterman, Jeffrey M
 ; TITLE OF INVENTION: Inhibition of Histone Deacetylase
 ; FILE REFERENCE: 106101.229
 ; CURRENT APPLICATION NUMBER: US/09/563,728A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/132,287
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: 1-4 and 23-26 are modified
 ; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
 ; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
 ; OTHER INFORMATION: deoxyribonucleotides
 US-09-563-728A-12

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 8;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
 |||||
 Db 26 GAATCCGCATGACTCATAACTGCTG 1

RESULT 10
 US-10-145-493B-82/c
 ; Sequence 82, Application US/10145493B
 ; Publication No. US20030096777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Besterman, Jeffrey
 ; APPLICANT: MacLeod, Robert
 ; APPLICANT: Siders, William
 ; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
 ; FILE REFERENCE: MET-015DV
 ; CURRENT APPLICATION NUMBER: US/10/145,493B
 ; CURRENT FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 09/420,692
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: US 60/104,804


```
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-82

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACCCATAATTGCTG 1

RESULT 11
US-10-145-493B-83/c
; Sequence 83, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-83

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACTCATAACTTGCTG 1

RESULT 12
US-10-145-493B-45/c
; Sequence 45, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-45

Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 13
US-09-563-728A-5/c
; Sequence 5, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-5

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 14
US-09-563-728A-14/c
; Sequence 14, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
```

; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-14

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 15

US-10-145-493B-55/c

; Sequence 55, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 55

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-55

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 16

US-10-145-493B-46/c

; Sequence 46, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 46

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-46

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTAATTATTATGGACA 187
Db 22 TTGGAATTAATTATTATGGACA 1

RESULT 17

US-10-145-493B-89/c

; Sequence 89, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 89

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-89

Query Match 1.4%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACCCATAACTTGCTG 1

RESULT 18

US-10-145-493B-53/c

; Sequence 53, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-53

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 16;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
|||||
Db 23 AAAGTCTGTACTACTACGACGG 1

RESULT 19
US-10-145-493B-54/c
; Sequence 54, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTACTATTATGGACA 187
|||||
Db 22 TTGGAATTACTATTATGGACA 1

RESULT 20
US-09-754-167-12/c
; Sequence 12, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGAGCAAGATGCGGCAGA 120
|||||
Db 20 GCGAGCAAGATGCGGCAGA 1

RESULT 21
US-09-754-167-13/c
; Sequence 13, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCTGTACTACT 153
|||||
Db 20 GAGGAAAGTCTGTACTACT 1

RESULT 22
US-09-754-167-14/c
; Sequence 14, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGTGCTGCTCAACTATGG 247
|||||
Db 20 AATTGTGCTGCTCAACTATGG 1

RESULT 23
US-09-754-167-15/c
; Sequence 15, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-15

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 GCTGCTCAACTATGGTCTCT 252
Db 20 GCTGCTCAACTATGGTCTCT 1

RESULT 24
US-09-754-167-16/c
; Sequence 16, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-16

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGGTCTCTACCGA 257
Db 20 TCAACTATGGTCTCTACCGA 1

RESULT 25
US-09-754-167-17/c
; Sequence 17, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGGTCTCTACCGAAAAAT 262
Db 20 TATGGTCTCTACCGAAAAAT 1

RESULT 26
US-09-754-167-18/c
; Sequence 18, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCTCACAAGCCCAATGC 292
Db 20 CGCCTCACAAGCCCAATGC 1

RESULT 27
US-09-754-167-19/c
; Sequence 19, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-19

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCCAATGCTGAGG 297
Db 20 TCACAAAGCCCAATGCTGAGG 1

RESULT 28
US-09-754-167-20/c
; Sequence 20, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-20

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      283 AAGCCAATGCTGAGGAGATG 302
      |||||||
Db      20 AAGCCAATGCTGAGGAGATG 1

RESULT 29
US-09-754-167-21/c
; Sequence 21, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-21

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      288 AATGCTGAGGAGATGACCAA 307
      |||||||
Db      20 AATGCTGAGGAGATGACCAA 1

RESULT 30
US-09-754-167-22/c
; Sequence 22, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-22

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      293 TGAGGAGATGACCAAGTACC 312
      |||||||
Db      20 TGAGGAGATGACCAAGTACC 1

RESULT 31
US-09-754-167-23/c
```

```
; Sequence 23, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-23

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      369 TACAGCAAGCAGATGCAGAG 388
      |||||||
Db      20 TACAGCAAGCAGATGCAGAG 1

RESULT 32
US-09-754-167-24/c
; Sequence 24, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-24

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      405 GACTGTCCAGTATTCGATGG 424
      |||||||
Db      20 GACTGTCCAGTATTCGATGG 1

RESULT 33
US-09-754-167-25/c
; Sequence 25, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```



```
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-25

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 TGTTGAGTTCTGTCAGTTG 446
      |||||
Db 20 TGTTGAGTTCTGTCAGTTG 1

RESULT 34
US-09-754-167-26/c
; Sequence 26, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-26

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 CTTAATAAGCAGCAGACGGA 499
      |||||
Db 20 CTTAATAAGCAGCAGACGGA 1

RESULT 35
US-09-754-167-27/c
; Sequence 27, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-27

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGACGGACATCG 504
      |||||
Db 20 TAAGCAGCAGACGGACATCG 1

RESULT 36
US-09-754-167-29/c
; Sequence 29, Application US/09754167
```

```
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-29

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 ATCGTCTTGGCCATCCTGGA 595
      |||||
Db 20 ATCGTCTTGGCCATCCTGGA 1

RESULT 37
US-09-754-167-30/c
; Sequence 30, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-30

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGCCCATCCTGGAATGC 600
      |||||
Db 20 CTTGCCCATCCTGGAATGC 1

RESULT 38
US-09-754-167-31/c
; Sequence 31, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```
US-09-754-167-31
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GCGGTGGAAGAGGCGCTTCTA 673
Db 20 GCGGTGGAAGAGGCGCTTCTA 1

RESULT 39
US-09-754-167-32/c
; Sequence 32, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-32
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 GAGGCGCTTCTACACCGGA 682
Db 20 GAGGCGCTTCTACACCGGA 1

RESULT 40
US-09-754-167-33/c
; Sequence 33, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-33
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 GGAGAGTACTTCCAGGAAC 733
Db 20 GGAGAGTACTTCCAGGAAC 1

RESULT 41
US-09-754-167-34/c
; Sequence 34, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-34
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCCAGGAAGTGGG 738
Db 20 GTACTTCCCAGGAAGTGGG 1

RESULT 42
US-09-754-167-35/c
; Sequence 35, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-35
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 TCCCAGGAAGTGGGACCTA 743
Db 20 TCCCAGGAAGTGGGACCTA 1

RESULT 43
US-09-754-167-36/c
; Sequence 36, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-36
```

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 GGAAGTGGGACCTACGGGA 748
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGAAGTGGGACCTACGGGA 1

RESULT 44
US-09-754-167-37/c
; Sequence 37, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-37

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTTAACTAC 788
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGTATTATGCTGTTAACTAC 1

RESULT 45
US-09-754-167-38/c
; Sequence 38, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-38

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CCCGCTCCGAGACGGGATTG 807
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCCGCTCCGAGACGGGATTG 1

RESULT 46
US-09-754-167-39/c
; Sequence 39, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-39

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCCTATGAGGCCATT 830
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ACGAGTCCTATGAGGCCATT 1

RESULT 47
US-09-754-167-40/c
; Sequence 40, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-40

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GTCATGTCCAAAGTAATGGA 859
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTCATGTCCAAAGTAATGGA 1

RESULT 48
US-09-754-167-41/c
; Sequence 41, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-41

```
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      845 GTCCAAAGTAATGGAGATGT 864
      |||||
Db      20 GTCCAAAGTAATGGAGATGT 1

RESULT 49
US-09-754-167-42/c
; Sequence 42, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      850 AAGTAATGGAGATGTTCCAG 869
      |||||
Db      20 AAGTAATGGAGATGTTCCAG 1

RESULT 50
US-09-754-167-43/c
; Sequence 43, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      859 AGATGTTCCAGCCTAGTCGC 878
      |||||
Db      20 AGATGTTCCAGCCTAGTCGC 1

RESULT 51
US-09-754-167-44/c
; Sequence 44, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
```

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; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-44

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      905 CCTATCTGGGATCGGTTAG 924
      |||||
Db      20 CCTATCTGGGATCGGTTAG 1

RESULT 52
US-09-754-167-45/c
; Sequence 45, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-45

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      918 CGGTTAGGTTGCTTCAATCT 937
      |||||
Db      20 CGGTTAGGTTGCTTCAATCT 1

RESULT 53
US-09-754-167-46/c
; Sequence 46, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-46

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 ATCAAAGGACACGCCAAGTG 961
|||||
Db 20 ATCAAAGGACACGCCAAGTG 1

RESULT 54
US-09-754-167-47/c
; Sequence 47, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-47

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 947 AGGACAGCGCCAAGTGTGTGG 966
|||||
Db 20 AGGACAGCGCCAAGTGTGTGG 1

RESULT 55
US-09-754-167-48/c
; Sequence 48, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-48

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 GAGGCGGTGGTTACACCAT 1025
|||||
Db 20 GAGGCGGTGGTTACACCAT 1

RESULT 56
US-09-754-167-49/c
; Sequence 49, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-49

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGGCCCTGGATAC 1075
|||||
Db 20 ACAGCTGTGGCCCTGGATAC 1

RESULT 57
US-09-754-167-50/c
; Sequence 50, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-50

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 ACAATGACTACTTTGAATAC 1118
|||||
Db 20 ACAATGACTACTTTGAATAC 1

RESULT 58
US-09-754-167-51/c
; Sequence 51, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-51

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
QY      1378 CTGAAGAGGAGGAGGAGGGG 1397
      |||||
Db      20 CTGAAGAGGAGGAGGAGGGG 1
      |||||

RESULT 64
US-09-754-167-58/c
; Sequence 58, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-58

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 GATGAAAAGAGAAAGACCC 1468
      |||||
Db      20 GATGAAAAGAGAAAGACCC 1
      |||||

RESULT 65
US-09-754-167-59/c
; Sequence 59, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-59

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1499 GAAAACCAAGGAGGAGAGC 1518
      |||||
Db      20 GAAAACCAAGGAGGAGAGC 1
      |||||

RESULT 66
US-09-754-167-60/c
; Sequence 60, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
```

```
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-60

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1504 CCAAGGAGGAGAGCCAGAA 1523
      |||||
Db      20 CCAAGGAGGAGAGCCAGAA 1
      |||||

RESULT 67
US-09-754-167-61/c
; Sequence 61, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-61

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1509 GAGGAGAGCCAGAGCCAA 1528
      |||||
Db      20 GAGGAGAGCCAGAGCCAA 1
      |||||

RESULT 68
US-09-754-167-62/c
; Sequence 62, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-62

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1514 GAAGCCAGAACCCAAAGGGG 1533
Db 20 GAAGCCAGAACCCAAAGGGG 1

RESULT 69
US-09-754-167-63/c
; Sequence 63, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-63

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGGCCTGAATGGACCT 1567
Db 20 AAGTTGGCCTGAATGGACCT 1

RESULT 70
US-09-754-167-64/c
; Sequence 64, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-64

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 71
US-09-817-913-17/c
; Sequence 17, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145

; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 72
US-09-817-913-18/c
; Sequence 18, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 73
US-09-817-538-17/c
; Sequence 17, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human

US-09-817-538-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604

Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 74

US-09-817-538-18/c
; Sequence 18, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584

Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 75

US-09-563-728A-1/c
; Sequence 1, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zuomei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604

Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 76
US-09-563-728A-10/c
; Sequence 10, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zuomei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-10

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604

Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 77

US-10-189-818B-8/c
; Sequence 8, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-8

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604

Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 78

US-10-189-818B-10/c

; Sequence 10, Application US/10189818B

; Publication No. US20040072770A1

; GENERAL INFORMATION:

; APPLICANT: BESTERMAN, JEFFREY M.

; APPLICANT: ZUOMEI, LI

; APPLICANT: DELORME, DANIEL

; APPLICANT: BONFILS, CLAIRE

; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8

; FILE REFERENCE: MET-024US1(1002/025)

; CURRENT APPLICATION NUMBER: US/10/189,818B

; CURRENT FILING DATE: 2002-07-03

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:

; OTHER INFORMATION: Synthetic oligonucleotide

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-189-818B-10

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584

Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 79

US-10-145-493B-35/c

; Sequence 35, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 35

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-35

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCGCTGGTGTGTCTC 36

Db 20 CCGCTGGTGTGTCTC 1

RESULT 80

US-10-145-493B-36/c

; Sequence 36, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 36

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-36

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCCACTCGGTTCAT 48

Db 20 GCTGTCTCCCACTCGGTTCAT 1

RESULT 81

US-10-145-493B-37/c

; Sequence 37, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 37

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-37

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCCACTCGGTTCATCC 50

Db 20 TGTCTCCCACTCGGTTCATCC 1

RESULT 82


```
US-10-145-493B-38/c
; Sequence 38, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-38
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCACTCGGTCATCCTG 52
Db 20 TCTCCACTCGGTCATCCTG 1

RESULT 83
US-10-145-493B-39/c
; Sequence 39, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-39
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTGAGAACACA 60
Db 20 TCGGTCATCCTGAGAACACA 1

RESULT 84
US-10-145-493B-41/c
; Sequence 41, Application US/10145493B
; Publication No. US20030096777A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-41
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 85
US-10-145-493B-43/c
; Sequence 43, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-43
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 86
US-10-145-493B-44/c
; Sequence 44, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
```

APPLICANT: Siders, William
TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
FILE REFERENCE: MET-015DV
CURRENT APPLICATION NUMBER: US/10/145,493B
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 09/420,692
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: US 60/104,804
PRIOR FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-145-493B-44

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 87

US-10-052-390B-1/c
Sequence 1, Application US/10052390B
Publication No. US20030148970A1
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffery M.
APPLICANT: Bonfils, Claire
APPLICANT: Li, Zuomei
APPLICANT: Woo, Soon H.
APPLICANT: Vaisburg, Arkadii
APPLICANT: Delorme, Daniel
APPLICANT: Fournel, Marielle
APPLICANT: Lavoie, Rico
TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
FILE REFERENCE: MET-004US1
CURRENT APPLICATION NUMBER: US/10/052,390B
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,674
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-052-390B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 88

US-10-052-390B-2/c
Sequence 2, Application US/10052390B
Publication No. US20030148970A1
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffery M.
APPLICANT: Bonfils, Claire
APPLICANT: Li, Zuomei
APPLICANT: Woo, Soon H.

APPLICANT: Vaisburg, Arkadii
APPLICANT: Delorme, Daniel
APPLICANT: Fournel, Marielle
APPLICANT: Lavoie, Rico
TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
FILE REFERENCE: MET-004US1
CURRENT APPLICATION NUMBER: US/10/052,390B
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,674
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 89

US-10-051-819B-1/c
Sequence 1, Application US/10051819B
Publication No. US20030152557A1
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffery M.
APPLICANT: Bonfils, Claire
APPLICANT: Li, Zuomei
APPLICANT: Woo, Soon
APPLICANT: Vaisburg, Arkadii
APPLICANT: Delorme, Daniel
APPLICANT: Fournel, Marielle
APPLICANT: Lavoie, Rico
TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
FILE REFERENCE: MET-002US1
CURRENT APPLICATION NUMBER: US/10/051,819B
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/261,674
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-051-819B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 90

US-10-051-819B-2/c
Sequence 2, Application US/10051819B
Publication No. US20030152557A1
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffery M.
APPLICANT: Bonfils, Claire
APPLICANT: Li, Zuomei
APPLICANT: Woo, Soon
APPLICANT: Vaisburg, Arkadii

APPLICANT: Delorme, Daniel
APPLICANT: Fournel, Marielle
APPLICANT: Lavoie, Rico
TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
FILE REFERENCE: MET-002US1
CURRENT APPLICATION NUMBER: US/10/051,819B
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/261,674
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-051-819B-2

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 91
US-09-733-692A-24/c
Sequence 24, Application US/09733692A
Patent No. US20020155581A1
GENERAL INFORMATION:
APPLICANT: Murphy, Brian R.
APPLICANT: Collins, Peter L.
APPLICANT: Schmidt, Alexander C.
APPLICANT: Durbin, Anna P.
APPLICANT: Skiadopoulos, Mario H.
APPLICANT: Tao, Tao
TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVS) AS
VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
BY PIV AND OTHER HUMAN PATHOGENS
FILE REFERENCE: 15280-404100US
CURRENT APPLICATION NUMBER: US/09/733,692A
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/170,195
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 24
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
OTHER INFORMATION: primer
US-09-733-692A-24

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTGATATTCCATGGTGACGGC 656
Db 24 ATTGCTATTCCATGCAGACGGC 1

RESULT 92
US-09-754-167-28/c
Sequence 28, Application US/09754167
Patent No. US20010019328A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION

FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-28

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 490 AGCAGACGACATCGCCGTG 509
Db 20 AGCAGACGACATCGCTGTG 1

RESULT 93
US-09-754-167-53/c
Sequence 53, Application US/09754167
Patent No. US20010019328A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 53
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-53

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1246 TCCAAACGACGCGATTCCT 1265
Db 20 TCCAAATGCAGCGATTCCT 1

RESULT 94
US-10-145-493B-40/c
Sequence 40, Application US/10145493B
Publication No. US20030096777A1
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffrey
APPLICANT: MacLeod, Robert
APPLICANT: Siders, William
TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
FILE REFERENCE: MET-015DV
CURRENT APPLICATION NUMBER: US/10/145,493B
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 09/420,692
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: US 60/104,804
PRIOR FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
SEQ ID NO 40
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

```
; OTHER INFORMATION: primer
US-10-145-493B-40

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGAGCGRCTCTGTCACTC 81
      ||||| ||||| ||||| |||||
Db      20 CCTGAGCGTCTCTGTCACTC 1

RESULT 95
US-10-145-493B-42/c
; Sequence 42, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-42

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1531 GGGTCAAGGAGGAGGCCAAG 1550
      ||||| ||||| ||||| |||||
Db      20 GGGTCAAGGAGGAGGTCAAG 1

RESULT 96
US-09-953-318-65/c
; Sequence 65, Application US/09953318
; Publication No. US20030105036A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-65

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      518 TGGGGGCCTGCACCATGCAA 537
```

```
      ||||| ||||| ||||| |||||
Db      20 TGGGAGCCTGCACCAAGCAA 1

RESULT 97
US-10-446-373-65/c
; Sequence 65, Application US/10446373
; Publication No. US20030204076A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/10/446,373
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-65

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      518 TGGGGGCCTGCACCATGCAA 537
      ||||| ||||| ||||| |||||
Db      20 TGGGAGCCTGCACCAAGCAA 1

RESULT 98
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-995-529-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 40;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1453 AAAAAGAGAAAGACCCA 1469
      ||||| ||||| ||||| |||||
Db      17 AAAAAGAGAAAGAYCCA 1

RESULT 99
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
```

APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-995-529-198

Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 40;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 100

US-09-996-263-13/c
Sequence 13, Application US/09996263
Publication No. US20030004325A1
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,263
FILING DATE: 28-No. US20030004325A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-996-263-13

Query Match 1.0%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 101

US-10-057-550-28/c
Sequence 28, Application US/10057550
Publication No. US20030032607A1
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/057,550
CURRENT FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: 09/506,073
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 09/143,214
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: PCT/US98/13961
PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: US 08/888,982
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: US 08/756,806
PRIOR FILING DATE: 1996-11-26
PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/250,856
PRIOR FILING DATE: 1994-05-31
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-10-057-550-28

Query Match

Best Local Similarity 1.0%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 102

US-10-173-225B-27/c
Sequence 27, Application US/10173225B
Publication No. US20030119769A1
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
FILE REFERENCE: ISPH-0665
CURRENT APPLICATION NUMBER: US/10/173,225B
CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US 10/057,550
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 09/143,214
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: PCT/US98/13961
PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: US 08/888,982
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: US 08/756,806
PRIOR FILING DATE: 1996-11-26
PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/250,856


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; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1507 AGGAGGAGAGCCAGAG 1524
      |||||
Db      19 AGGAGGAGAGCCAGCAG 2

RESULT 103
US-10-352-586-13/c
; Sequence 13, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; FILE REFERENCE: ISIS5137
; CURRENT APPLICATION NUMBER: US/10/352,586
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 09/389,283
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-352-586-13

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1507 AGGAGGAGAGCCAGAG 1524
      |||||
Db      19 AGGAGGAGAGCCAGCAG 2

RESULT 104
US-10-293-863-27/c
; Sequence 27, Application US/10293863
; Publication No. US20040092464A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 11
; FILE REFERENCE: HTS-0090
; CURRENT APPLICATION NUMBER: US/10/293,863
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-863-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
```

```

Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1512 GACAAGCCAGAGCCAAA 1529
      |||||
Db      19 GTGAAGCCAGAGCCAAA 2

RESULT 105
US-10-293-863-61
; Sequence 61, Application US/10293863
; Publication No. US20040092464A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 11
; FILE REFERENCE: HTS-0090
; CURRENT APPLICATION NUMBER: US/10/293,863
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-863-61

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1512 GACAAGCCAGAGCCAAA 1529
      |||||
Db      2 GTGAAGCCAGAGCCAAA 19

RESULT 106
US-10-349-143-5052/c
; Sequence 5052, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5052
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-20549 for SEQ 1118,
US-10-349-143-5052

Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1469 AGAGGAGAGAGGAGGAA 1485
```

```
Db      17 AGAGGAGAGATGGAA 1
|||||
RESULT 107
US-09-923-246-23
; Sequence 23, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-923-246-23
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGGACTGC 18
|||||

RESULT 108
US-10-295-723-23
; Sequence 23, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; TITLE OF INVENTION: NOVEL CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-22
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGGACTGC 18
|||||

RESULT 110
US-10-243-072-39
; Sequence 39, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
```

```

; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-39

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGACTGC 18

RESULT 111
US-10-414-186-22
; Sequence 22, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGACTGC 18

RESULT 112
US-10-414-186-22
; Sequence 22, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGACTGC 18

RESULT 113
US-10-414-186-39
; Sequence 39, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-39

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCCTGC 528
Db      1 ACTGGGCTGGGGACTGC 18

RESULT 113
US-10-659-684-23
; Sequence 23, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-659-684-23
```

OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-659-684-23

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
| | | | | | | | | | | | | | | | | |
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 114
US-09-935-868-3/c
; Sequence 3, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-09-935-868-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
| | | | | | | | | | | | | | | | | |
Db 16 CACCATGGTGCGGCG 1

RESULT 115
US-10-287-035-3/c
; Sequence 3, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-287-035-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
| | | | | | | | | | | | | | | | | |
Db 16 CACCATGGTGCGGCG 1

RESULT 116
US-10-282-162-3/c
; Sequence 3, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-282-162-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
| | | | | | | | | | | | | | | | | |
Db 16 CACCATGGTGCGGCG 1

RESULT 117
US-10-138-674-5827
; Sequence 5827, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions i
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 70;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCGCTGCACCA 532
| | | | | | | | | | | | | | | | | |

Db 1 CUGGAGCCUGCACCA 16

RESULT 118

US-10-287-949A-5827

; Sequence 5827, Application US/10287949A

; Publication No. US20040102389A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MEHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/287,949A

; CURRENT FILING DATE: 2003-04-11

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5827

; LENGTH: 16

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-287-949A-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 70;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532

|||||

Db 1 CUGGAGCCUGCACCA 16

RESULT 119

US-09-866-108-971/c

; Sequence 971, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 971

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-971

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 79;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCCTG 527

|||||

Db 17 TTGGGCTGGGGCCTG 2

RESULT 120

US-09-866-108-972/c

; Sequence 972, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine


```
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-972

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      512 TTGGGCTGGGGCCTG 527
Db      16 TTGGCTTGGGGCCTG 1

RESULT 121
US-09-780-164-387/c
; Sequence 387, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 387
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-387

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1119 TTGGACCAGATTTC A 1134
Db      17 TTGGACCAGATTGCA 2

RESULT 122
US-09-780-164-966/c
; Sequence 966, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 966
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-966

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1119 TTGGACCAGATTTC A 1134
```

```
Db      16 TTGGACCAGATTGCA 1

RESULT 123
US-10-138-674-4754
; Sequence 4754, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4754

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      517 CTGGGGGCTGCACCA 532
Db      1 CUGGGAGCCUGCACCA 16

RESULT 124
US-10-138-674-7632
; Sequence 7632, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7632

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      516 GCTGGGGGCTGCACC 531
Db      2 GCUGGGAGCCUGCACCC 17

RESULT 125
US-10-287-949A-4754
; Sequence 4754, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4754

```

```

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

```

```

RESULT 126
US-10-287-949A-7632
; Sequence 7632, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7632

```

```

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 516 GCTGGGGCGCTGCACC 531
Db 2 GCUGGAGCCUGCACCC 17

```

```

RESULT 127
US-09-861-779-4/c
; Sequence 4, Application US/09861779
; Publication No. US20030191280A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: Class II Cytokine Receptor-7
; FILE REFERENCE: 96-24C2
; CURRENT APPLICATION NUMBER: US/09/861,779

```

```

; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 08/943,087
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 08/803,305
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-779-4

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
Db 17 AAAGAGAAACACCCAG 2

RESULT 128
US-10-636-716-4/c
; Sequence 4, Application US/10636716
; Publication No. US20040072229A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other

```

```

; IMMEDIATE SOURCE:
; CLONE: ZC11107
US-10-636-716-4

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
Db 17 AAAGAGAAACACCCAG 2

RESULT 129
US-10-269-557-46
; Sequence 46, Application US/10269557
; Publication No. US2003009664A1
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/10/269,557
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/207,388
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Used to clone Neisseria meningitidis Hsp70
; OTHER INFORMATION: gene and to construct Neisseria meningitidis Hsp70
; OTHER INFORMATION: expression vectors
US-10-269-557-46

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 283 AAGCCATGCTGAGGA 298
Db 2 AAGCCATGCCGAGGA 17

RESULT 130
US-10-367-438-165
; Sequence 165, Application US/10367438
; Publication No. US20030180773A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, Daniel
; BLUMENFELD, Marta
; TCHOUMAKOV, Ilia
; TITLE OF INVENTION: Biallelic markers for use in
; constructing a high density disequilibrium map of
; the human genome.
; NUMBER OF SEQUENCES: 336
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 550 West C Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/10/367,438
; FILING DATE: 14-Feb-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,075A
; FILING DATE: 14-Jan-2000
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-10-367-438-165

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAG 1472
Db 1 AGAGAAAGAACCCAGAG 16

RESULT 131
US-10-349-143-4102
; Sequence 4102, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4102
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13273 for SEQ 168,
US-10-349-143-4102

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTCTGGGTCTCTG 16
Db 1 ATGTCTGGGTCTCTG 16

RESULT 132
US-10-349-143-9179
; Sequence 9179, Application US/10349143
; Publication No. US20040005584A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9179
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-2275 for SEQ 1314, in compleme
US-10-349-143-9179
```

```

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY 1457 AGAGAAAGACCCAGAG 1472
Db 1 AGAGAAAGACCCAGAG 16
```

```

RESULT 133
US-09-866-108-6562
; Sequence 6562, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
```

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6562
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6562
```

```

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY 1058 AGCTGTGGCCCTGGATA 1074
Db 1 ACCTCTGGCCCTGGATA 17
```

```

RESULT 134
US-09-866-108-7084
; Sequence 7084, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
```

; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7084
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7084

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGGC 1518
| | | | | | | | | | | | | | | | | | |
Db 1 AGCCAAGGAGGAGGC 17

RESULT 135
US-09-866-108-8667
; Sequence 8667, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8667

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAG 1517
| | | | | | | | | | | | | | | | | | |
Db 1 AAGCCAAGAGGAGGAGAG 17

RESULT 136
US-09-866-108-8668
; Sequence 8668, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8668
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8668

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGAGC 1518
| | | | | | | | | | | | | | | | | | |
Db 1 AGCCAAGAGGAGGAGAGC 17

RESULT 137
US-09-961-077-117
; Sequence 117, Application US/09961077
; Publication No. US20030014775A1

GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-09-961-077-117
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 495 ACGGACATCGCGTGAA 511
Db 1 AAGUACAUCGCCGUGAA 17
RESULT 138
US-09-784-674-66/c
Sequence 66, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Delenstarr, Glenda C.

Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 20BQ
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-784-674-66
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GTCTGGGGTCTCTGCCC 19
Db 17 GTCTGGGTCTCTGCCC 1
RESULT 139
US-09-877-478-438/c
Sequence 438, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09

```

; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
; ORGANISM: Hepatitis B virus
US-09-877-478-438

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 AGAAGCCAGAGCCAAA 1529
Db 17 AGAAGTCAGAGGCCAAA 1

RESULT 140
US-09-848-754A-3128
; Sequence 3128, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3128
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-848-754A-3128

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 160 GGGATGTTGGAAATTAC 176
Db 1 GGGAAUUUGGAAAUUAC 17

RESULT 141
US-09-827-395A-723/c
; Sequence 723, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-827-395A-723

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 GTCCGAGGCATCTGGCT 558
Db 17 GTCAGCGGCATCTGGCT 1

RESULT 142
US-09-740-332-1709/c
; Sequence 1709, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1709
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1709

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 CTGAGGAGATGACCAAG 308
Db 17 CTGAGGAGCTGGCCAAG 1

RESULT 143
US-09-740-332-1724
; Sequence 1724, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1724
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1724

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
```

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1153 CCAATATGACTAACCAG 1169
||||:||||:||||
Db 1 CCAUAUGACUCCCCAG 17

RESULT 144
US-09-740-332-2831/c
; Sequence 2831, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2831
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2831

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 CAATATGACTAACCAG 1170
|||||||:||||
Db 17 CAATATGACTCCCCAGA 1

RESULT 145
US-09-740-332-2846
; Sequence 2846, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2846

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 291 GCTGAGGAGATGACAA 307
||:|||||:||||
Db 1 GCUGAGGAGCUGGCCAA 17

RESULT 146
US-09-740-332-4133

; Sequence 4133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4133

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1267 AGGACGCCATCCCTGAG 1283
|||||||:||||
Db 1 AGGACCCCGACCCUGAG 17

RESULT 147
US-09-792-818-95
; Sequence 95, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-95

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGACCTCTCCAGCTCTG 1578
||||:||||:||||
Db 1 GGACUUCUCCAUUCUG 17

RESULT 148
US-09-817-879-1709/c
; Sequence 1709, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879

; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1709
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1709

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 CTCGAGGAGATGACCAAG 308
|||||
Db 17 CTGAGAGCTGGCCAAG 1

RESULT 149
US-09-817-879-1724
; Sequence 1724, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MEHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1724
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1724

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1153 CCAATATGACTAACCAG 1169
|||||
Db 1 CCAUAUGACUCCCCAG 17

RESULT 150
US-09-817-879-2831/C
; Sequence 2831, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MEHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2831
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2831

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 CAATATGACTAACCAGA 1170
|||||
Db 17 CAATATGACTCCCCAGA 1

RESULT 151
US-09-817-879-2846
; Sequence 2846, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MEHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2846

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 291 GCTGAGGAGATGACCAA 307
|||||
Db 1 GCUGAGGAGCUGGCCAA 17

RESULT 152
US-09-817-879-4133
; Sequence 4133, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MEHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4133

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1267 AGGACGCCATCCTGAG 1283

Db 1 AGGACCCACCCUGAG 17
RESULT 153
US-10-342-902-438/c
; Sequence 438, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-438

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 AGAAGCCAGAGCCAA 1529
Db 17 AGAAGTCAGAGGCAA 1

RESULT 154
US-09-949-298-2
; Sequence 2, Application US/09949298
; Publication No. US20020104107A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: LESTER, Henry A.
; APPLICANT: LABARCA, Cesar
; APPLICANT: SCHWARZ, Johannes
; APPLICANT: Fonck, Carlos
; TITLE OF INVENTION: POINT MUTANT MICE WITH HYPERSENSITIVE ALPHA 4 NICOTINIC RECEPTORS
; FILE REFERENCE: CIT1400-1
; CURRENT APPLICATION NUMBER: US/09/949,298
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230,757
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mouse
US-09-949-298-2

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 GGTGCTGCTGTCTCCCA 39
Db 1 GGTGCTGCTTTCTCTCA 17
RESULT 155
US-09-927-046-108/c
; Sequence 108, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-108

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAGAGAT 390
Db 17 CAAACAGATACAGAGAT 1

RESULT 156
US-10-430-882-723/c
; Sequence 723, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
; LENGTH: 17
; TYPE: RNA


```
; ORGANISM: Homo sapiens
US-10-430-882-723

Query Match          0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 GTCCGAGGCATCTGGCT 558
Db 17 GTCAGCGGCATCTGGCT 1

RESULT 157
US-10-060-756A-588
; Sequence 588, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 588
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-588

Query Match          0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1456 AAGAGAAAGACCCAGAG 1472
Db 1 AAGAGGAAGACCTAGAG 17

RESULT 158
US-10-060-756A-589
; Sequence 589, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 589
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-589

Query Match          0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAGG 1473
Db 1 AGAGGAAGACCTAGAGG 17

RESULT 159
US-10-060-756A-590
; Sequence 590, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 590
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-590

Query Match          0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1458 GAGAAAGACCCAGAGGA 1474
Db 1 GAGGAAGACCTAGAGGA 17

RESULT 160
US-10-060-756A-591
; Sequence 591, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
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US-10-060-756A-591

US-10-060-998-1329

US-10-163-552-559

```
; ORGANISM: Homo sapiens
US-10-156-306-4966

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 CCCGCTGGTGTGCTGT 33
Db 17 CCTGCTGGAGCTGCTGT 1

RESULT 165
US-10-156-306-5928
; Sequence 5928, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5928
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5928

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 365 GGAGTACAGCAAGCAGA 381
Db 1 GGAGUACAGCAACUGA 17

RESULT 166
US-10-156-306-6988
; Sequence 6988, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6988
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6988

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1534 TCAAGGAGGAGGCCAAG 1550
Db 1 UGAAGGAGGAGGCCCGAG 17

RESULT 167
US-10-238-700-3037
; Sequence 3037, Application US/10238700
```

```
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3037
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3037

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAGGACGAAGACGACCC 1312
Db 1 GUGGACGAUACGACCC 17

RESULT 168
US-10-238-700-3128
; Sequence 3128, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3128
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3128

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 658 TGAAGAGCGCCTTCTAC 674
Db 1 UGGAGGAUGCCUUCUAC 17

RESULT 169
US-10-339-782-240/c
; Sequence 240, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
```

; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-240

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGTACTGGAGAAGATC 1196
Db 17 AGTTCTTGGAGAAGATC 1

RESULT 170
US-10-297-068-971/c
; Sequence 971, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-971

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CACTCGGTATCCTGAG 54
Db 17 CACTCGGTACGCTGTG 1

RESULT 171
US-10-138-674-947
; Sequence 947, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 947
; LENGTH: 17
; TYPE: RNA

; ORGANISM: Homo sapiens
US-10-138-674-947

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAACTGCTGTGAAACTT 482
Db 1 CAACUGCUUUGAAACUU 17

RESULT 172
US-10-138-674-2635/c
; Sequence 2635, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2635
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2635

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGTC 34
Db 17 CTGCTGGTGTGCTGTC 1

RESULT 173
US-10-138-674-4755
; Sequence 4755, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4755

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCGCTGCACCATG 534

Db 1 UGGAGCCUGCAACAAG 17

RESULT 174

US-10-138-674-4756

; Sequence 4756, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4756

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-138-674-4756

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 95;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCGTCGACCATGCAA 537

Db 1 GAGCCUGCAACAAGCAA 17

RESULT 175

US-10-138-674-4757

; Sequence 4757, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4757

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-138-674-4757

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 95;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAAG 539

Db 1 GCCUGCAACAAGCAAGG 17

RESULT 176

US-10-138-674-4758

; Sequence 4758, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4758

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-138-674-4758

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 95;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAGA 540

Db 1 CCUGCAACAAGCAAGGA 17

RESULT 177

US-10-138-674-5394/c

; Sequence 5394, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5394

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-138-674-5394

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 95;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGGTGAGGACTGTCC 412

Db 17 GGTGGAGAGGACTGTCC 1

RESULT 178

US-10-138-674-7633

; Sequence 7633, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7633

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 519 GGGGCGCTGCACCATGC 535
||| |||:|||||||
Db 1 GGGAGCCUGCACCACG 17

RESULT 179

US-10-287-949A-947
; Sequence 947, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 947
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-947

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 95;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAAACTT 482
||| |||:|||||:
Db 1 CAACUGCUUUGAAACUU 17

RESULT 180

US-10-287-949A-2635/c
; Sequence 2635, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2635
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-2635

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 CCGCTGCTGCTGCTGTC 34
|||||:|||||
Db 17 CTGCTGCTGATGCTGTC 1

RESULT 181

US-10-287-949A-4755
; Sequence 4755, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4755

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGCGCTGCACCATG 534
:|||||:|||||
Db 1 UGGGAGCCUGCACCACG 17

RESULT 182

US-10-287-949A-4756
; Sequence 4756, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4756
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4756

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCCTGCACCATGCAA 537
|||||:|||||
Db 1 GAGCCUGCACCACGCAA 17

RESULT 183

US-10-287-949A-4757
; Sequence 4757, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4757
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4757

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAG 539
|||:|||||
Db 1 GCCUGCACCAAGCAAGG 17

RESULT 184

US-10-287-949A-4758
; Sequence 4758, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4758
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4758

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAGA 540
||:|||||
Db 1 CCUGCACCAAGCAAGGA 17

RESULT 185

US-10-287-949A-5394/c
; Sequence 5394, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5394
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5394

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGGTGAGGACTGTCC 412
|||:|||||
Db 17 GGTGGAGAGGACTGTCC 1

RESULT 186

US-10-287-949A-7633
; Sequence 7633, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7633

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 519 GGGGGCCTGCACCATGC 535
|||:|||||
Db 1 GGGAGCCUGCACCAAGC 17

RESULT 187

US-10-712-672-978/c
; Sequence 978, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 978
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-978

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 665 GGCCTTCTACACCGG 681
Db 17 GGCCTTCTGACCGG 1

RESULT 188
US-10-712-672-2255/c
Sequence 2255, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrira, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBH00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2255
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-2255

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1459 AGAAGACCCAGGAG 1475
Db 17 AGAAGACCCCTGAGCAG 1

RESULT 189
US-10-287-919-1912/c
Sequence 1912, Application US/10287919
Publication No. US20030085830A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SEQ ID NO 1912
LENGTH: 15
TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome.
FEATURE:
LOCATION: (1132255)...(1132269)
OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1912

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1255 AGCGATTCCTGAGG 1269
Db 15 AGGAGATTCCTGAGG 1

RESULT 190
US-10-287-919-1925/c
Sequence 1925, Application US/10287919
Publication No. US20030085830A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SEQ ID NO 1925
LENGTH: 15
TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome.
FEATURE:
LOCATION: (1144469)...(1144482)
OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1925

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1255 AGCGATTCCTGAGG 1269
Db 15 AGGAGATTCCTGAGG 1

RESULT 191
US-09-420-433-19/c
Sequence 19, Application US/09420433
Patent No. US20020098480A1
GENERAL INFORMATION:
APPLICANT: Sidransky, David
TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
TITLE OF INVENTION: HISTOLOGIC TISSUE
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/420,433
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/181,664
FILING DATE: JANUARY 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3055
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..16
US-09-420-433-19

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 111 ATGGCGCAGACGCG 125
Db 15 ATGGCGCAGACGCG 1

RESULT 192
US-09-945-505-18/c
Sequence 18, Application US/09945505
Publication No. US20030165844A1
GENERAL INFORMATION:
APPLICANT: Anastasio, Alison E.
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Nandabalan, Krishnan
APPLICANT: Parks, Katie E.
APPLICANT: Stephens, J. Claiborne
TITLE OF INVENTION: Haplotypes of the TNFRSF1A Gene
FILE REFERENCE: MWH-0030US
CURRENT APPLICATION NUMBER: US/09/945,505
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-945-505-18

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 94;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1331 CTGCTCCTCTGACAA 1345
Db 15 CYGCTCCTCTGACCA 1

RESULT 193
US-10-056-414-258
Sequence 258, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-056-414-258

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 94;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1045 GGACATATGAGAC 1057
Db 2 GGACAUAGAGAC 14

RESULT 194
US-10-043-875-250/c
Sequence 250, Application US/10043875
Publication No. US20030054339A1
GENERAL INFORMATION:
APPLICANT: De Smet, Koenraad
APPLICANT: Stuyver, Lieven
TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Revertant
TITLE OF INVENTION: Transcriptase Gene
FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
CURRENT APPLICATION NUMBER: US/10/043,875
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 60/286,102
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: EP 01870085.6
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: EP 01870005.4
PRIOR FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 884
SOFTWARE: PatentIn version 3.1
SEQ ID NO 250
LENGTH: 15
TYPE: DNA
ORGANISM: Human immunodeficiency virus
US-10-043-875-250

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1273 CCATCCCTGAGGA 1285
Db 15 CCATCCCTGAGGA 3

RESULT 195
US-10-101-030B-48/c
; Sequence 48, Application US/10101030B
; Publication No. US20030113738A1
; GENERAL INFORMATION:
; APPLICANT: Liu, et al.
; TITLE OF INVENTION: Evolving New Molecular Function
; FILE REFERENCE: 0342941-0071
; CURRENT APPLICATION NUMBER: US/10/101,030B
; CURRENT FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer
US-10-101-030B-48

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CGCTGGTGCTGCT 31
Db 15 CGCTGGTGCTGCT 3

RESULT 196
US-10-084-839-3505/c
; Sequence 3505, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3505

; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3505

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 14 CAAGCAGATGCAG 2

RESULT 197
US-10-084-839-3483/c
; Sequence 3483, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3483
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3483

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 14 CAAGCAGATGCAG 2

RESULT 198
US-10-084-839-3501/c
; Sequence 3501, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:

APPLICANT: Third Wave Technologies
APPLICANT: Allawi, Hatim
APPLICANT: Argue, Brad T.
APPLICANT: Bartholomay, Christian T.
APPLICANT: Chehak, LuAnne
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lymaicheva, Natalie E.
APPLICANT: Ma, WuPo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3501
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3501

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 13 CAAGCAGATGCAG 1

RESULT 199
US-10-277-216-330/c
Sequence 330, Application US/10277216
Publication No. US2004002470A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 2976-4051
CURRENT APPLICATION NUMBER: US/10/277,216
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 10/126,022
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 330
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-277-216-330

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1

RESULT 200
US-10-126-022-330/c
Sequence 330, Application US/10126022
Publication No. US20040023215A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 2976-4039US2
CURRENT APPLICATION NUMBER: US/10/126,022
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 330
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-126-022-330

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1

RESULT 201
US-08-591-486B-124
Sequence 124, Application US/08591486B
Publication No. US20020037866A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg F
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Gotingen, Wolfgang Brysch
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treat
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh Street, N.W.
CITY: Washington, D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93111059.7
;; FILING DATE: 10-JUL-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP94/02218
;; FILING DATE: 6-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10496/P60122
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 638-6666
;; TELEFAX: (202) 393-9350
;; TELEX: RCA 248593 IDEA UR
;; INFORMATION FOR SEQ ID NO: 124:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
US-08-591-486B-124

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred.No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 202
US-09-739-928-11
; Sequence 11, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutuyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamber, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-739-928-11

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred.No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1184 CCTGGAGAAGATCAAA 1199
Db 1 CCAGCAGAAGATCAAA 16

RESULT 203
US-10-339-674-569/c
; Sequence 569, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 569
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (633528)...(633543)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-339-674-569
ConnectronObjectNumber = 76

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred.No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 CATTTCAGCCGGTC 842
Db 16 CACTTTCAGCCGGTC 1

RESULT 204
US-10-059-888-22
; Sequence 22, Application US/10059888
; Publication No. US20030025882A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,888
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-888-22
```

```
Query Match          0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1385 GGAGGGGAGAGGGGGC 1400
      ||||| |||||
Db 1 GGAGGGGGGGGGGGC 16
```

RESULT 205

```
US-10-059-877-22
; Sequence 22, Application US/10059877
; Publication No. US20030157490A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,877
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-877-22
```

```
Query Match          0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1385 GGAGGGGAGAGGGGGC 1400
      ||||| |||||
Db 1 GGAGGGGGGGGGGGC 16
```

RESULT 206

```
US-10-065-133A-35
; Sequence 35, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
```

```
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-065-133A-35
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Query Match          0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 207

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; Sequence 35, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
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; Sequence 5988, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5988
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Job time : 5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:19:55 ; Search time 8 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 449 seqs, 9636 residues

Total number of hits satisfying chosen parameters: 898

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Post-processing: Minimum Match 0%
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Listing first 449 summaries

Database : rnmpm2.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	26	1.6	26	1 US-09-563-728A-4	Sequence 4, Appli
C 5	26	1.6	26	1 US-09-563-728A-13	Sequence 13, Appl
C 6	26	1.6	26	1 US-10-145-493B-47	Sequence 47, Appl
C 7	26	1.6	26	1 US-10-154-659-17	Sequence 17, Appl
C 8	25.2	1.6	30	1 US-10-189-818B-39	Sequence 39, Appl
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C 111	22.8	1.4	26	1	US-10-145-493B-55	Sequence 55, Appl	C 184	20	1.2	20	1	PCT-US01-46518A-17	Sequence 17, Appl
C 112	22.4	1.4	25	1	US-60-507-511-89132	Sequence 89132, A	C 185	20	1.2	20	1	PCT-US01-46518A-18	Sequence 18, Appl
C 113	22	1.4	22	1	US-09-420-692A-46	Sequence 46, Appl	C 186	20	1.2	20	1	PCT-US01-46518A-19	Sequence 19, Appl
C 114	22	1.4	22	1	US-10-145-493B-46	Sequence 46, Appl	C 187	20	1.2	20	1	PCT-US01-46518A-20	Sequence 20, Appl
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C 139	21.8	1.4	25	1	US-60-507-511-67531	Sequence 67531, A	C 212	20	1.2	20	1	PCT-US01-46518A-46	Sequence 46, Appl
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C 146	21.8	1.4	26	1	US-10-145-493B-89	Sequence 89, Appl	C 219	20	1.2	20	1	PCT-US01-46518A-54	Sequence 54, Appl
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C 163	20.2	1.3	25	1	US-09-954-427A-233681	Sequence 233681, A	C 236	20	1.2	20	1	US-09-420-692A-43	Sequence 43, Appl
C 164	20.2	1.3	25	1	US-09-954-429-3060	Sequence 3060, Ap	C 237	20	1.2	20	1	US-09-420-692A-44	Sequence 44, Appl
C 165	20.2	1.3	25	1	US-09-954-429B-3060	Sequence 3060, Ap	C 238	20	1.2	20	1	US-09-563-728A-1	Sequence 1, Appl
C 166	20.2	1.3	25	1	US-10-719-956-140528	Sequence 140528, A	C 239	20	1.2	20	1	US-09-563-728A-10	Sequence 10, Appl
C 167	20.2	1.3	25	1	US-10-719-956-319560	Sequence 319560, A	C 240	20	1.2	20	1	US-09-754-167-12	Sequence 12, Appl
C 168	20.2	1.3	25	1	US-10-719-956-356287	Sequence 356287, A	C 241	20	1.2	20	1	US-09-754-167-13	Sequence 13, Appl
C 169	20.2	1.3	25	1	US-10-719-956-417657	Sequence 417657, A	C 242	20	1.2	20	1	US-09-754-167-14	Sequence 14, Appl
C 170	20.2	1.3	25	1	US-10-719-956-444838	Sequence 444838, A	C 243	20	1.2	20	1	US-09-754-167-15	Sequence 15, Appl
C 171	20.2	1.3	25	1	US-60-233-166-71840	Sequence 71840, A	C 244	20	1.2	20	1	US-09-754-167-16	Sequence 16, Appl
C 172	20.2	1.3	25	1	US-60-427-836-140528	Sequence 140528, A	C 245	20	1.2	20	1	US-09-754-167-17	Sequence 17, Appl
C 173	20.2	1.3	25	1	US-60-427-836-319560	Sequence 319560, A	C 246	20	1.2	20	1	US-09-754-167-18	Sequence 18, Appl
C 174	20.2	1.3	25	1	US-60-427-836-356287	Sequence 356287, A	C 247	20	1.2	20	1	US-09-754-167-19	Sequence 19, Appl
C 175	20.2	1.3	25	1	US-60-427-836-417657	Sequence 417657, A	C 248	20	1.2	20	1	US-09-754-167-20	Sequence 20, Appl
C 176	20.2	1.3	25	1	US-60-427-836-444838	Sequence 444838, A	C 249	20	1.2	20	1	US-09-754-167-21	Sequence 21, Appl
C 177	20.2	1.3	25	1	US-60-507-511-178470	Sequence 178470, A	C 250	20	1.2	20	1	US-09-754-167-22	Sequence 22, Appl
C 178	20.2	1.3	25	1	US-60-507-511-178471	Sequence 178471, A	C 251	20	1.2	20	1	US-09-754-167-23	Sequence 23, Appl
C 179	20	1.2	20	1	PCT-US01-46518A-12	Sequence 12, Appl	C 252	20	1.2	20	1	US-09-754-167-24	Sequence 24, Appl

399 14.4 0.9 16 1 US-10-287-949A-5827 Sequence 5827, Ap
400 14.4 0.9 16 1 US-10-310-188-39096 Sequence 39096, A
C 401 14.4 0.9 17 1 PCT-US01-29656-779 Sequence 779, App
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403 14.4 0.9 17 1 PCT-US02-17674-678 Sequence 678, App
C 404 14.4 0.9 17 1 PCT-US02-25940-19155 Sequence 19155, A
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C 407 14.4 0.9 17 1 US-09-546-745A-3282 Sequence 3282, Ap
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C 411 14.4 0.9 17 1 US-09-780-164-387 Sequence 387, App
C 412 14.4 0.9 17 1 US-09-780-164-966 Sequence 966, App
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420 14.4 0.9 17 1 US-10-287-949A-4754 Sequence 4754, Ap
421 14.4 0.9 17 1 US-10-287-949A-7632 Sequence 7632, Ap
C 422 14.4 0.9 17 1 US-10-310-188-18308 Sequence 18308, A
423 14.4 0.9 17 1 US-10-367-892-19155 Sequence 19155, A
C 424 14.4 0.9 17 1 US-10-723-361-971 Sequence 971, App
C 425 14.4 0.9 17 1 US-10-723-361-972 Sequence 972, App
C 426 14.4 0.9 17 1 US-60-315-676-779 Sequence 779, App
C 427 14.4 0.9 17 1 US-60-315-676-780 Sequence 780, App
C 428 14.4 0.9 17 1 US-60-339-764-2348 Sequence 2348, Ap
C 429 14.4 0.9 17 1 US-60-339-764-2349 Sequence 2349, Ap
C 430 14.4 0.9 17 1 US-08-406-779-74 Sequence 74, Appli
C 431 14.4 0.9 18 1 US-08-803-305-4 Sequence 4, Appli
C 432 14.4 0.9 18 1 US-08-803-305A-4 Sequence 4, Appli
C 433 14.4 0.9 18 1 US-09-275-712-4 Sequence 4, Appli
C 434 14.4 0.9 18 1 US-09-463-075A-165 Sequence 165, App
435 14.4 0.9 18 1 US-10-269-557-46 Sequence 46, Appl
C 436 14.4 0.9 18 1 US-10-303-778-7630 Sequence 7630, Ap
437 14.4 0.9 18 1 US-10-303-778-8260 Sequence 8260, Ap
438 14.4 0.9 18 1 US-10-310-188-14763 Sequence 14763, A
439 14.4 0.9 18 1 US-10-310-188-18291 Sequence 18291, A
440 14.4 0.9 18 1 US-10-310-188-29093 Sequence 29093, A
C 441 14.4 0.9 18 1 US-10-310-188-35240 Sequence 35240, A
442 14.4 0.9 18 1 US-10-310-188-86025 Sequence 86025, A
443 14.4 0.9 18 1 US-10-310-188-86059 Sequence 86059, A
444 14.4 0.9 18 1 US-10-349-143-4102 Sequence 4102, Ap
445 14.4 0.9 18 1 US-10-349-143-9179 Sequence 9179, Ap
446 14.4 0.9 18 1 US-10-349-143-9179 Sequence 165, App
447 14.4 0.9 18 1 US-10-367-438-165 Sequence 4, Appli
C 448 14.4 0.9 18 1 US-10-636-716-4 Sequence 2026, Ap
449 14.4 0.9 18 1 US-60-082-614-2026

ALIGNMENTS

RESULT 1
US-09-574-376B-170
; Sequence 170, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Shah, Nila
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 31
; TYPE: DNA

; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-170

Query Match 1.9%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 22;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGTACTTCCCGAGGAAGTGGGACCTACGGGA 748
Db 1 AGTACTTCCCGAGGAAYTGGGACCTACGGGA 31

RESULT 2

US-09-574-376B-173
; Sequence 173, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Shah, Nila
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-173

Query Match 1.9%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 22;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1334 CTCCTCTGACAAACGATTCCTGTGAGGAA 1364
Db 1 CTCCTCTGACAAACGATTCCTGTGAGGAA 31

RESULT 3

US-09-420-692A-47/c
; Sequence 47, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-47

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

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C 254	20	1.2	1	US-09-754-167-26	Sequence 26, Appl	C 327	16.8	1.0	20	1	PCT-US02-29148-65	Sequence 65, Appl
C 255	20	1.2	1	US-09-754-167-27	Sequence 27, Appl	328	16.8	1.0	20	1	US-09-514-000-14731	Sequence 14731, A
C 256	20	1.2	1	US-09-754-167-29	Sequence 29, Appl	C 329	16.8	1.0	20	1	US-09-953-318-65	Sequence 65, Appl
C 257	20	1.2	1	US-09-754-167-30	Sequence 30, Appl	C 330	16.8	1.0	20	1	US-10-446-373-65	Sequence 65, Appl
C 258	20	1.2	1	US-09-754-167-31	Sequence 31, Appl	331	16.8	1.0	21	1	US-10-310-188-35269	Sequence 35269, A
C 259	20	1.2	1	US-09-754-167-32	Sequence 32, Appl	332	16.8	1.0	21	1	US-10-751-736-12071	Sequence 12071, A
C 260	20	1.2	1	US-09-754-167-33	Sequence 33, Appl	333	16.8	1.0	21	1	US-10-751-736-28225	Sequence 28225, A
C 261	20	1.2	1	US-09-754-167-34	Sequence 34, Appl	334	16.8	1.0	21	1	US-10-751-736-28228	Sequence 28228, A
C 262	20	1.2	1	US-09-754-167-35	Sequence 35, Appl	C 335	16.6	1.0	17	1	PCT-US02-38147-198	Sequence 198, App
C 263	20	1.2	1	US-09-754-167-36	Sequence 36, Appl	C 336	16.6	1.0	17	1	US-09-995-529-198	Sequence 198, App
C 264	20	1.2	1	US-09-754-167-37	Sequence 37, Appl	C 337	16.6	1.0	17	1	US-10-011-250-198	Sequence 198, App
C 265	20	1.2	1	US-09-754-167-38	Sequence 38, Appl	338	16.4	1.0	18	1	US-10-310-188-43026	Sequence 43026, A
C 266	20	1.2	1	US-09-754-167-39	Sequence 39, Appl	C 339	16.4	1.0	20	1	PCT-US03-35845-27	Sequence 27, Appl
C 267	20	1.2	1	US-09-754-167-40	Sequence 40, Appl	340	16.4	1.0	20	1	PCT-US03-35845-61	Sequence 61, Appl
C 268	20	1.2	1	US-09-754-167-41	Sequence 41, Appl	C 341	16.4	1.0	20	1	US-08-465-866B-13	Sequence 13, Appl
C 269	20	1.2	1	US-09-754-167-42	Sequence 42, Appl	C 342	16.4	1.0	20	1	US-08-756-806-27	Sequence 27, Appl
C 270	20	1.2	1	US-09-754-167-43	Sequence 43, Appl	C 343	16.4	1.0	20	1	US-09-996-263-13	Sequence 13, Appl
C 271	20	1.2	1	US-09-754-167-44	Sequence 44, Appl	C 344	16.4	1.0	20	1	US-10-057-550-28	Sequence 28, Appl
C 272	20	1.2	1	US-09-754-167-45	Sequence 45, Appl	C 345	16.4	1.0	20	1	US-10-057-550A-27	Sequence 27, Appl
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C 274	20	1.2	1	US-09-754-167-47	Sequence 47, Appl	C 347	16.4	1.0	20	1	US-10-266-090-45347	Sequence 45347, A
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C 279	20	1.2	1	US-09-754-167-52	Sequence 52, Appl	352	15.8	1.0	19	1	US-10-125-568-24	Sequence 24, Appl
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C 282	20	1.2	1	US-09-754-167-56	Sequence 56, Appl	C 355	15.4	1.0	17	1	US-09-546-745A-3283	Sequence 3283, Ap
C 283	20	1.2	1	US-09-754-167-57	Sequence 57, Appl	C 356	15.4	1.0	17	1	US-09-546-745A-3284	Sequence 3284, Ap
C 284	20	1.2	1	US-09-754-167-58	Sequence 58, Appl	C 357	15.4	1.0	17	1	US-10-227-563-16869	Sequence 16869, A
C 285	20	1.2	1	US-09-754-167-59	Sequence 59, Appl	C 358	15.4	1.0	17	1	US-10-367-892-16869	Sequence 16869, A
C 286	20	1.2	1	US-09-754-167-60	Sequence 60, Appl	C 359	15.4	1.0	18	1	PCT-US00-00654-44	Sequence 44, Appl
C 287	20	1.2	1	US-09-754-167-61	Sequence 61, Appl	C 360	15.4	1.0	18	1	US-09-913-684-44	Sequence 44, Appl
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C 289	20	1.2	1	US-09-754-167-63	Sequence 63, Appl	362	15.4	1.0	19	1	PCT-US03-05044-34	Sequence 34, Appl
C 290	20	1.2	1	US-09-754-167-64	Sequence 64, Appl	C 363	15.4	1.0	19	1	PCT-US03-05044-311	Sequence 311, App
C 291	20	1.2	1	US-09-817-538-17	Sequence 17, Appl	C 364	15	0.9	16	1	US-10-310-188-16111	Sequence 16111, A
C 292	20	1.2	1	US-09-817-538-18	Sequence 18, Appl	C 365	15	0.9	18	1	US-10-266-090-38180	Sequence 38180, A
C 293	20	1.2	1	US-09-817-913-17	Sequence 17, Appl	366	14.8	0.9	18	1	PCT-US00-06067-23	Sequence 23, Appl
C 294	20	1.2	1	US-09-817-913-18	Sequence 18, Appl	C 367	14.8	0.9	18	1	US-08-282-197B-14	Sequence 14, Appl
C 295	20	1.2	1	US-10-051-819B-1	Sequence 1, Appli	368	14.8	0.9	18	1	US-09-159-254-22	Sequence 22, Appl
C 296	20	1.2	1	US-10-051-819B-2	Sequence 2, Appli	C 369	14.8	0.9	18	1	US-09-264-908-22	Sequence 22, Appl
C 297	20	1.2	1	US-10-052-390B-1	Sequence 1, Appli	370	14.8	0.9	18	1	US-09-264-908-39	Sequence 39, Appl
C 298	20	1.2	1	US-10-052-390B-2	Sequence 2, Appli	371	14.8	0.9	18	1	US-09-265-117-22	Sequence 22, Appl
C 299	20	1.2	1	US-10-145-493B-35	Sequence 35, Appl	372	14.8	0.9	18	1	US-09-265-117-39	Sequence 39, Appl
C 300	20	1.2	1	US-10-145-493B-36	Sequence 36, Appl	373	14.8	0.9	18	1	US-09-265-992-23	Sequence 23, Appl
C 301	20	1.2	1	US-10-145-493B-37	Sequence 37, Appl	374	14.8	0.9	18	1	US-09-347-930-22	Sequence 22, Appl
C 302	20	1.2	1	US-10-145-493B-38	Sequence 38, Appl	375	14.8	0.9	18	1	US-09-347-930-39	Sequence 39, Appl
C 303	20	1.2	1	US-10-145-493B-39	Sequence 39, Appl	376	14.8	0.9	18	1	US-09-628-127-22	Sequence 22, Appl
C 304	20	1.2	1	US-10-145-493B-41	Sequence 41, Appl	377	14.8	0.9	18	1	US-09-628-127-39	Sequence 39, Appl
C 305	20	1.2	1	US-10-145-493B-43	Sequence 43, Appl	378	14.8	0.9	18	1	US-10-243-072-22	Sequence 22, Appl
C 306	20	1.2	1	US-10-145-493B-44	Sequence 44, Appl	379	14.8	0.9	18	1	US-10-243-072-39	Sequence 39, Appl
C 307	20	1.2	1	US-10-154-659-15	Sequence 15, Appl	C 380	14.8	0.9	18	1	US-10-310-188-23157	Sequence 23157, A
C 308	20	1.2	1	US-10-189-818B-8	Sequence 8, Appli	C 381	14.8	0.9	18	1	US-10-310-188-23178	Sequence 23178, A
C 309	20	1.2	1	US-10-189-818B-10	Sequence 10, Appl	C 382	14.8	0.9	18	1	US-10-310-188-58290	Sequence 58290, A
C 310	19.4	1.2	1	US-10-751-736-43855	Sequence 43855, A	383	14.8	0.9	18	1	US-10-310-188-86028	Sequence 86028, A
C 311	19.2	1.2	1	US-09-458-813-25	Sequence 25, Appl	384	14.8	0.9	18	1	US-10-414-186-22	Sequence 22, Appl
C 312	19.2	1.2	1	US-09-459-062-18	Sequence 18, Appl	385	14.8	0.9	18	1	US-10-414-186-39	Sequence 39, Appl
C 313	19.2	1.2	1	US-09-733-692A-24	Sequence 24, Appl	386	14.8	0.9	18	1	US-10-659-684-23	Sequence 23, Appl
C 314	18.4	1.1	1	PCT-US01-46518A-28	Sequence 28, Appl	387	14.8	0.9	18	1	US-10-715-998-22	Sequence 22, Appl
C 315	18.4	1.1	1	PCT-US01-46518A-53	Sequence 53, Appl	388	14.8	0.9	18	1	US-10-715-998-39	Sequence 39, Appl
C 316	18.4	1.1	1	US-09-420-692A-40	Sequence 40, Appl	C 389	14.4	0.9	16	1	US-08-563-105-3	Sequence 3, Appli
C 317	18.4	1.1	1	US-09-420-692A-42	Sequence 42, Appl	C 390	14.4	0.9	16	1	US-09-177-009-3	Sequence 3, Appli
C 318	18.4	1.1	1	US-09-754-167-28	Sequence 28, Appl	391	14.4	0.9	16	1	US-09-708-690-5827	Sequence 5827, Ap
C 319	18.4	1.1	1	US-09-754-167-53	Sequence 53, Appl	C 392	14.4	0.9	16	1	US-09-787-835-3	Sequence 3, Appli
C 320	18.4	1.1	1	US-10-145-493B-40	Sequence 40, Appl	393	14.4	0.9	16	1	US-09-870-161-5827	Sequence 3, Appli
C 321	18.4	1.1	1	US-10-145-493B-42	Sequence 42, Appl	C 394	14.4	0.9	16	1	US-09-935-868-3	Sequence 3, Appli
C 322	18	1.1	1	US-10-154-659-12	Sequence 12, Appl	395	14.4	0.9	16	1	US-10-138-674-5827	Sequence 5827, Ap
C 323	17.8	1.1	1	US-10-751-736-43856	Sequence 43856, A	C 396	14.4	0.9	16	1	US-10-138-674A-5827	Sequence 3, Appl
C 324	17.4	1.1	1	US-10-266-090-51356	Sequence 51356, A	C 397	14.4	0.9	16	1	US-10-282-162-3	Sequence 3, Appli
C 325	17	1.1	1	PCT-US98-04571A-122	Sequence 122, App	C 398	14.4	0.9	16	1	US-10-287-035-3	Sequence 3, Appli

; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFELS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACETYLASE-7 AND 8
; FILE REFERENCE: NET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-189-818B-39

Query Match 1.6%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GTCAAGGAGGAGGCCAAGTTGGCCTGAATG 1562
Db 30 GTCAAGGAGGAGGTCGACTTGGCCTGAATG 1

RESULT 9
US-09-396-196F-102090
; Sequence 102090, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102090
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102090

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AATGGAATCTATCGCCCTCACAA 284
Db 1 AATGGAATCTATCGCCCTCACAA 25

RESULT 10
US-09-396-196F-102091
; Sequence 102091, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102091

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TGGAAATCTATCGCCCTCACAAAGC 286
Db 1 TGGAAATCTATCGCCCTCACAAAGC 25

RESULT 11
US-09-396-196F-102092
; Sequence 102092, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102092

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 GCGCTCCATCCGTCAGATAACATG 362
Db 1 GCGCTCCATCCGTCAGATAACATG 25

RESULT 12
US-09-396-196F-102093
; Sequence 102093, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102093

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-563-728A-4/c
; Sequence 4, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-4

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 5
US-09-563-728A-13/c
; Sequence 13, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-13

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 6
US-10-145-493B-47/c

; Sequence 47, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-47

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 7
US-10-154-659-17
; Sequence 17, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; TITLE OF INVENTION: Genes regulated by trapoxin-induced HDAC inhibition
; FILE REFERENCE: 4-32017A
; CURRENT APPLICATION NUMBER: US/10/154,659
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-154-659-17

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1312 CTGACAAGCGCATCTCGATCTGCTCC 1337
Db 1 CTGACAAGCGCATCTCGATCTGCTCC 26

RESULT 8
US-10-189-818B-39/c
; Sequence 39, Application US/10189818B

QY 342 TCCATCCGTCACAGATAACATGTCGG 366
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATCCGTCACAGATAACATGTCGG 25

RESULT 13
US-09-396-196F-102094
; Sequence 102094, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102094

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TCCGTCACAGATAACATGTCGGAGTA 370
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCGTCACAGATAACATGTCGGAGTA 25

RESULT 14
US-09-396-196F-102095
; Sequence 102095, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102095

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 CGTCCAGATAACATGTCGGAGTACA 372
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CGTCCAGATAACATGTCGGAGTACA 25

RESULT 15
US-09-396-196F-102096
; Sequence 102096, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102096

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 TCTGTCAGTTGTCTACTGGTGGTTC 460
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCTGTCAGTTGTCTACTGGTGGTTC 25

RESULT 16
US-09-396-196F-102097
; Sequence 102097, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102097
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102097

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 TGTGTCAGTTGTCTACTGGTGGTTCG 462
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TGTGTCAGTTGTCTACTGGTGGTTCG 25

RESULT 17
US-09-396-196F-102098
; Sequence 102098, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 102098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102098

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      440 TCAGTTGTCTACTGGTGGTCTCTGTG 464
      |||||
Db      1 TCAGTTGTCTACTGGTGGTCTCTGTG 25

RESULT 18
US-09-396-196F-102099
; Sequence 102099, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102099

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      442 AGTTGTCTACTGGTGGTCTCTGTGGC 466
      |||||
Db      1 AGTTGTCTACTGGTGGTCTCTGTGGC 25

RESULT 19
US-09-396-196F-102100
; Sequence 102100, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102100

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      448 CTAAGTGGTGGTCTCTGTGGCAAGTGC 472
      |||||
Db      1 CTAAGTGGTGGTCTCTGTGGCAAGTGC 472

RESULT 20
US-09-396-196F-102101
; Sequence 102101, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102101

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      450 ACTGGTGGTCTCTGTGGCAAGTGTG 474
      |||||
Db      1 ACTGGTGGTCTCTGTGGCAAGTGTG 25

RESULT 21
US-09-396-196F-102102
; Sequence 102102, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102102

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      272 TCGCCCTCACAAAGCCCAATGCTGAG 296
      |||||
Db      1 TCGCCCTCACAAAGCCCAATGCTGAG 25

RESULT 22
US-09-396-196F-102103
; Sequence 102103, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
```

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; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102103

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 CCTCACAAGCCCAATGCTGAGGAGA 300
Db 1 CCTCACAAGCCCAATGCTGAGGAGA 25

RESULT 23
US-09-396-196F-102104
; Sequence 102104, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102104

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAGCCCAATGCTGAGGAGATG 302
Db 1 TCACAAGCCCAATGCTGAGGAGATG 25

RESULT 24
US-09-396-196F-102105
; Sequence 102105, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102105

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAGCCCAATGCTGAGGAGATG 302
Db 1 TCACAAGCCCAATGCTGAGGAGATG 25

RESULT 25
US-09-396-196F-102106
; Sequence 102106, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102106
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102106

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ACTACATTAATTTCTGCGCTCCAT 346
Db 1 ACTACATTAATTTCTGCGCTCCAT 25

RESULT 26
US-09-396-196F-102107
; Sequence 102107, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102107

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 TTAATTTCTTGGCTCCATCCGTCC 352
Db 1 TTAATTTCTTGGCTCCATCCGTCC 25
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; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126541

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 TCTTGGCCATCCTGGAAGTCTGCTAAA 604
Db 1 TCTTGGCCATCCTGGAAGTCTGCTAAA 25

RESULT 30
US-09-396-196F-126542
; Sequence 126542, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126542

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 TGGCCATCCTGGAAGTCTGCTAAAAGTA 607
Db 1 TGGCCATCCTGGAAGTCTGCTAAAAGTA 25

RESULT 31
US-09-396-196G-102090
; Sequence 102090, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102090
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus

```

```

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102108
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102108

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 AAATTCTTGGCTCCATCCGTCAG 354
Db 1 AAATTCTTGGCTCCATCCGTCAG 25

RESULT 28
US-09-396-196F-102109
; Sequence 102109, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102109

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 ATTCTTGGCTCCATCCGTCAGAT 356
Db 1 ATTCTTGGCTCCATCCGTCAGAT 25

RESULT 29
US-09-396-196F-126541
; Sequence 126541, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

```

```
US-09-396-196G-102090
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AATGAAATCTATCGCCCTCAGAAA 284
      |||||
Db 1 AATGAAATCTATCGCCCTCAGAAA 25

RESULT 32
US-09-396-196G-102091
; Sequence 102091, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102091

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TGGAAATCTATCGCCCTCAGAAAAGC 286
      |||||
Db 1 TGGAAATCTATCGCCCTCAGAAAAGC 25

RESULT 33
US-09-396-196G-102092
; Sequence 102092, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102092

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 GCGCTCCATCGTCCAGATAACATG 362
      |||||
Db 1 GCGCTCCATCGTCCAGATAACATG 25
```

```
US-09-396-196G-102093
; Sequence 102093, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102093

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCATCCGTCAGATAACATGTCGG 366
      |||||
Db 1 TCCATCCGTCAGATAACATGTCGG 25

RESULT 35
US-09-396-196G-102094
; Sequence 102094, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102094

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TCCGTCAGATAACATGTCGGAGTA 370
      |||||
Db 1 TCCGTCAGATAACATGTCGGAGTA 25

RESULT 36
US-09-396-196G-102095
; Sequence 102095, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
```



```
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102095
```

```
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      348 CGTCCAGATAACATGTCGGAGTACA 372
      |||||
Db      1 CGTCCAGATAACATGTCGGAGTACA 25
```

```
RESULT 37
US-09-396-196G-102096
; Sequence 102096, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102096
```

```
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      436 TCTGTCAAGTGTCTACTGGTGGTTC 460
      |||||
Db      1 TCTGTCAAGTGTCTACTGGTGGTTC 25
```

```
RESULT 38
US-09-396-196G-102097
; Sequence 102097, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102097
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102097
```

```
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      438 TGTCAAGTTGTCTACTGGTGGTTCG 462
      |||||
Db      1 TGTCAAGTTGTCTACTGGTGGTTCG 25
```

```
RESULT 39
US-09-396-196G-102098
; Sequence 102098, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102098
```

```
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      440 TCAGTTGTCTACTGGTGGTTCGTCG 464
      |||||
Db      1 TCAGTTGTCTACTGGTGGTTCGTCG 25
```

```
RESULT 40
US-09-396-196G-102099
; Sequence 102099, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102099
```

```
Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      442 AGTTGTCTACTGGTGGTTCGTGGC 466
      |||||
Db      1 AGTTGTCTACTGGTGGTTCGTGGC 25
```

```
RESULT 41
US-09-396-196G-102100
```

```
; Sequence 102100, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102100

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 CTACTGGTGGTCTGTGGCAAGTGC 472
DB 1 CTACTGGTGGTCTGTGGCAAGTGC 25

RESULT 42
US-09-396-196G-102101
; Sequence 102101, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102101

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 ACTGGTGGTCTGTGGCAAGTGTG 474
DB 1 ACTGGTGGTCTGTGGCAAGTGTG 25

RESULT 43
US-09-396-196G-102102
; Sequence 102102, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102102

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 ACTGGTGGTCTGTGGCAAGTGTG 474
DB 1 ACTGGTGGTCTGTGGCAAGTGTG 25

RESULT 44
US-09-396-196G-102103
; Sequence 102103, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102103

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 TCGCCCTCACAAGCCCAATGCTGAG 296
DB 1 TCGCCCTCACAAGCCCAATGCTGAG 25

RESULT 45
US-09-396-196G-102104
; Sequence 102104, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102104

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCCAATGCTGAGGAGATG 302
|||||
Db 1 TCACAAAGCCCAATGCTGAGGAGATG 25

RESULT 46
US-09-396-196G-102105
; Sequence 102105, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102105

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 ACCACAGCGATGACTACATTAAT 334
|||||
Db 1 ACCACAGCGATGACTACATTAAT 25

RESULT 47
US-09-396-196G-102106
; Sequence 102106, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102106
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102106

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ACTACATTAATTTCTGGCTCCAT 346
|||||
Db 1 ACTACATTAATTTCTGGCTCCAT 25

RESULT 48
US-09-396-196G-102107
; Sequence 102107, Application US/09396196G
; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102107

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 TTAATTTCTGGCTCCATCCGTCC 352
|||||
Db 1 TTAATTTCTGGCTCCATCCGTCC 25

RESULT 49
US-09-396-196G-102108
; Sequence 102108, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102108
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102108

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 AAATTTCTGGCTCCATCCGTCCAG 354
|||||
Db 1 AAATTTCTGGCTCCATCCGTCCAG 25

RESULT 50
US-09-396-196G-102109
; Sequence 102109, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102109

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 ATTCTGGCGTCCATCCGTCAGAT 356
Db 1 ATTCTGGCGTCCATCCGTCAGAT 25

RESULT 51
US-09-396-196G-126541
; Sequence 126541, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126541

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 580 TCTTGGCCATCTCGAACTGCTAAA 604
Db 1 TCTTGGCCATCTCGAACTGCTAAA 25

RESULT 52
US-09-396-196G-126542
; Sequence 126542, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126542

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 580 TCTTGGCCATCTCGAACTGCTAAA 604
Db 1 TCTTGGCCATCTCGAACTGCTAAA 25

RESULT 53
US-09-953-115A-21870
; Sequence 21870, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21870

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1297 AGGACGAAGACGACCCCTGACAAGCG 1321
Db 1 AGGACGAAGACGACCCCTGACAAGCG 25

RESULT 54
US-09-953-115A-21871
; Sequence 21871, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21871

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1312 CTGACAAGCGCATCTCGATCTGCTC 1336
Db 1 CTGACAAGCGCATCTCGATCTGCTC 25

RESULT 55
US-09-953-115A-21872
; Sequence 21872, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
```

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Qy 583 TGGCCATCCTGGAACTGCTAAAGTA 607
Db 1 TGGCCATCCTGGAACTGCTAAAGTA 25

RESULT 53
US-09-953-115A-21870
; Sequence 21870, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21870

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1297 AGGACGAAGACGACCCCTGACAAGCG 1321
Db 1 AGGACGAAGACGACCCCTGACAAGCG 25

RESULT 54
US-09-953-115A-21871
; Sequence 21871, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21871

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1312 CTGACAAGCGCATCTCGATCTGCTC 1336
Db 1 CTGACAAGCGCATCTCGATCTGCTC 25

RESULT 55
US-09-953-115A-21872
; Sequence 21872, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
```

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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21872

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1324 TCTCGATCTGCTCTCTCTGACAAACG 1348
      |||
      1 TCTCGATCTGCTCTCTCTGACAAACG 25
DB

RESULT 56
US-09-953-115A-21873
; Sequence 21873, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21873

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCCTGTGAGGAAGAGTTCTCCG 1374
      |||
      1 ATTGCCTGTGAGGAAGAGTTCTCCG 25
DB

RESULT 57
US-09-953-115A-21874
; Sequence 21874, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21874

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTGAATGGACCTCTCCAGCTCTGG 1579
      |||
      1 CCTGAATGGACCTCTCCAGCTCTGG 25
DB

RESULT 58
US-09-953-115A-21876
; Sequence 21876, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21876

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CTCTGACAAACGAATTCCTGTGAG 1361
      |||
      1 CTCTGACAAACGAATTCCTGTGAG 25
DB

RESULT 59
US-09-953-115A-21877
; Sequence 21877, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21877
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21877

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1074 ACGGAGATCCCTAATGAGCTTCCAT 1098
      |||
      1 ACGGAGATCCCTAATGAGCTTCCAT 25
DB

RESULT 60
US-09-953-115A-21878
; Sequence 21878, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21878
```


Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1210 TTGAGAACCTTAGAATGCTGCGCA 1234
|||||
Db 1 TTGAGAACCTTAGAATGCTGCGCA 25

RESULT 61
US-09-953-115A-21879
; Sequence 21879, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21879
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21879

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 982 TTAACCTGCCTATGCTGATGCTGGG 1006
|||||
Db 1 TTAACCTGCCTATGCTGATGCTGGG 25

RESULT 62
US-09-953-115A-21880
; Sequence 21880, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21880
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21880

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1094 TCCATACAATGACTACTTTGAATAC 1118
|||||
Db 1 TCCATACAATGACTACTTTGAATAC 25

RESULT 63
US-09-953-115A-21881
; Sequence 21881, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1

; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21881
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21881

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 TTTGTCAAGAGCTTTAAACCTGCCTA 993
|||||
Db 1 TTTGTCAAGAGCTTTAAACCTGCCTA 25

RESULT 64
US-09-953-115A-21882
; Sequence 21882, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21882

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 TTCAAGCTCCACATCAGTCCTTCCA 1155
|||||
Db 1 TTCAAGCTCCACATCAGTCCTTCCA 25

RESULT 65
US-09-953-115A-21883
; Sequence 21883, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21883

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TCCAATATGACTAACCAACACGA 1176

Db 1 TCCAATATGACTAACCAGAACGCA 25
RESULT 66
US-09-953-115A-21884
; Sequence 21884, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21884
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21884
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1168 AGAACACGAATGAGTACCTGGAGAA 1192
Db 1 AGAACACGAATGAGTACCTGGAGAA 25
RESULT 67
US-09-953-115A-21885
; Sequence 21885, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21885
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21885
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1413 TCCAACCTCAAAAAAGCCAGAGAG 1437
Db 1 TCCAACCTCAAAAAAGCCAGAGAG 25
RESULT 68
US-60-507-511-94242/c
; Sequence 94242, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 94242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-94242
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 GTCATCCTGAGAACACAGCCTGAGC 68
Db 25 GTCATCCTGAGAACACAGCCTGAGC 1
RESULT 69
US-60-507-511-122445/c
; Sequence 122445, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-122445
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 TGCTGCTGTCTCCCACTCGGTGATC 49
Db 25 TGCTGCTGTCTCCCACTCGGTGATC 1
RESULT 70
US-60-507-511-137223/c
; Sequence 137223, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-137223
Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 TCCCACTCGGTGATCCTGAGAACAC 59
Db 25 TCCCACTCGGTGATCCTGAGAACAC 1
RESULT 71
US-60-507-511-158029/c

```
; Sequence 158029, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158029
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-158029

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      39 ACTCGGTGTCCTGAGACACAGCC 63
Db      25 ACTCGGTGTCCTGAGACACAGCC 1

RESULT 72
US-09-420-692A-90/c
; Sequence 90, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-90

Query Match      1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      212 AATCCGCATGACTCATAATTGCTG 236
Db      25 AATCCGCATGACTCATAATTGCTG 1

RESULT 73
US-10-145-493B-90/c
; Sequence 90, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
```

```
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-90

Query Match      1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      212 AATCCGCATGACTCATAATTGCTG 236
Db      25 AATCCGCATGACTCATAATTGCTG 1

RESULT 74
US-09-563-728A-2/c
; Sequence 2, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-2

Query Match      1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      211 GAATCCGCATGACTCATAATTGCTG 236
Db      26 GAATCCGCATGACCCATAATTGCTG 1

RESULT 75
US-09-563-728A-3/c
; Sequence 3, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
```

; OTHER INFORMATION: oligonucleotide
US-09-563-728A-3

Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||
Db 26 GAATCCGCATGACTCATAACTTGCTG 1

RESULT 76
US-09-563-728A-11/c
; Sequence 11, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-11

Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||
Db 26 GAATCCGCATGACCCATAATTGCTG 1

RESULT 77
US-09-563-728A-12/c
; Sequence 12, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides

US-09-563-728A-12

Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||
Db 26 GAATCCGCATGACTCATAACTTGCTG 1

RESULT 78
US-09-396-196F-126540
; Sequence 126540, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126540

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 ATATCGTCTTGGCCCATCTGGAACT 598
|||
Db 1 ACATCGTCTTGGCCCATCTGGAACT 25

RESULT 79
US-09-396-196F-126543
; Sequence 126543, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126543
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126543

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 586 CCATCCTGGAAGTCTAAAGTATCA 610
|||
Db 1 CCATCCTGGAAGTCTAAAGTACCA 25

```

RESULT 80
US-09-396-196F-126544
; Sequence 126544, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126544
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126544

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 598 TGCTAAAGTATCACCAGAGGGTGCT 622
Db 1 TGCTAAAGTACCACCAGAGGGTGCT 25

RESULT 81
US-09-396-196F-126553
; Sequence 126553, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126553

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 550 CATCTGGCTTCTGTACGTCAATGA 574
Db 1 CATCCGGCTTCTGTACGTCAATGA 25

RESULT 82
US-09-396-196F-126555
; Sequence 126555, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126555
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126555

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GTTACGTCAATGATATCGTCTTGGC 586
Db 1 GTTACGTCAATGATATCGTCTTGGC 25

RESULT 83
US-09-396-196F-126556
; Sequence 126556, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126556

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCAATGATATCGT 580
Db 1 GCTTCTGTACGTCAATGATATCGT 25

RESULT 84
US-09-396-196F-126557
; Sequence 126557, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126557
```



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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126553

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 550 CATCTGGCTTCTGTACGTCAATGA 574
Db 1 CATCCGGCTTCTGTACGTCAATGA 25

RESULT 90
US-09-396-196G-126555
; Sequence 126555, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126555
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126555

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCAATGATATCGT 580
Db 1 GCTTCTGTACGTCAATGATATCGT 25

RESULT 91
US-09-396-196G-126556
; Sequence 126556, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126556

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 555 GCTTCTGTACGTCAATGATATCGT 580
Db 1 GCTTCTGTACGTCAATGATATCGT 25

RESULT 92
US-09-396-196G-126557
; Sequence 126557, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126557

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 565 ACGTCAATGATATCGTCTTGCCCAT 589
Db 1 ACGTCAATGATATCGTCTTGCCCAT 25

RESULT 93
US-09-396-196G-126558
; Sequence 126558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126558

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATATCGTCTTGCCCATCCT 592
Db 1 TCAATGATATCGTCTTGCCCATCCT 25

RESULT 94
US-09-396-196G-126559
; Sequence 126559, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126559
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126559

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 569 TCAATGATATCGTCTTGCCCATCCT 593
Db 1 TCAATGATATCGTCTTGCCCATCCT 25
```

```

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GTTACGTCAATGATATCGTCTTGCC 586
Db 1 GTTACGTCAATGATATCGTCTTGCC 25

RESULT 92
US-09-396-196G-126557
; Sequence 126557, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126557

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 565 ACGTCAATGATATCGTCTTGCCCAT 589
Db 1 ACGTCAATGATATCGTCTTGCCCAT 25

RESULT 93
US-09-396-196G-126558
; Sequence 126558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126558

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATATCGTCTTGCCCATCCT 592
Db 1 TCAATGATATCGTCTTGCCCATCCT 25

RESULT 94
US-09-396-196G-126559
; Sequence 126559, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126559
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126559

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 569 TCAATGATATCGTCTTGCCCATCCT 593
Db 1 TCAATGATATCGTCTTGCCCATCCT 25
```

APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Analysis of Human Genes
FILE REFERENCE: 3111.1
CURRENT APPLICATION NUMBER: US/09/953,115A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/232,597
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 33029
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 21875
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-09-953-115A-21875

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 GTCCAAACGCGGCGATTCCTGAGG 1269
Db 1 GTCCAAATGCAGGCGATTCCTGAGG 25

RESULT 95
US-10-719-956-181945
Sequence 181945, Application US/10719956
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 181945
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-181945

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCAATGAT 575
Db 1 ATCCGGCTTCTGTACGTCAATGAT 25

RESULT 96
US-10-719-956-337747
Sequence 337747, Application US/10719956
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 337747
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-337747

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 297 GAGATGACCAAGTACCACAGCGATG 321
Db 1 GAGATGACCAAGTACCACAGCGACG 25

RESULT 97
US-60-427-836-181945
Sequence 181945, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 181945
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-60-427-836-181945

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCAATGAT 575
Db 1 ATCCGGCTTCTGTACGTCAATGAT 25

RESULT 98
US-60-427-836-337747
Sequence 337747, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 337747
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-60-427-836-337747

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 297 GAGATGACCAAGTACCACAGCGATG 321
Db 1 GAGATGACCAAGTACCACAGCGACG 25

RESULT 99
US-60-507-511-59988/c
Sequence 59988, Application US/60507511
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: AM 101081
CURRENT APPLICATION NUMBER: US/60/507,511
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 203623
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59988

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-59988

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 TGAGACACAGCCTGAGCGRCTCTG 75
Db 25 TGAGACACAGCCTGAGCGTCTCTG 1

RESULT 100
US-60-507-511-76813/c
; Sequence 76813, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-76813

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 TCTGTCACTCGGGGTAGACCACGCG 96
Db 25 TCTGTCACTCGGGGTAGACCACGCG 1

RESULT 101
US-60-507-511-138258/c
; Sequence 138258, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-138258

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 AACACAGCCTGAGCGRCTCTGTCTAC 79
Db 25 AACACAGCCTGAGCGTCTCTGTCTAC 1

RESULT 102
US-09-420-692A-82/c
; Sequence 82, Application US/09420692A
```

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; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-82

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATATAATTGCTG 236
Db 25 AATCCGCATGACCCATAATTGCTG 1

RESULT 103
US-09-420-692A-83/c
; Sequence 83, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-83

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATATAATTGCTG 236
Db 25 AATCCGCATGACTCATATAACTTGTG 1

RESULT 104
US-10-145-493B-82/c
; Sequence 82, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
```

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; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-82

Query Match          1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACCCATAATTGCTG 1

RESULT 105
US-10-145-493B-83/c
; Sequence 83, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-83

Query Match          1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
Db 25 AATCCGCATGACTCATAACTTGCTG 1

RESULT 106
US-09-420-692A-45/c
; Sequence 45, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 23
```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-45

Query Match          1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
Db 23 AAAGTCTGTACTACTACGACGG 1

RESULT 107
US-10-145-493B-45/c
; Sequence 45, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-45

Query Match          1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
Db 23 AAAGTCTGTACTACTACGACGG 1

RESULT 108
US-09-420-692A-55/c
; Sequence 55, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-55

Query Match          1.4%; Score 22.8; DB 1; Length 26;
```


Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 109
US-09-563-728A-5/c
; Sequence 5, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-5
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 110
US-09-563-728A-14/c
; Sequence 14, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-14
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236

Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 111
US-10-145-493B-55/c
; Sequence 55, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; OTHER INFORMATION: primer
US-10-145-493B-55
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 112
US-60-507-511-89132/c
; Sequence 89132, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89132
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: primer
US-60-507-511-89132
Query Match 1.4%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 96;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 60 AGCCTGAGCGCTCTGTCACTCGG 83
Db 25 AGCCTGAGCGCTCTGTCACTCGG 2
RESULT 113
US-09-420-692A-46/c
; Sequence 46, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William

```
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-46

Query Match          1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      166 TTGGAATTAATTACTATTATGGACA 187
Db      22 TTGGAATTAATTACTATTATGGACA 1

RESULT 114
US-10-145-493B-46/c
; Sequence 46, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-46

Query Match          1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      166 TTGGAATTAATTACTATTATGGACA 187
Db      22 TTGGAATTAATTACTATTATGGACA 1

RESULT 115
US-09-396-196F-126545
; Sequence 126545, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
```

```
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126545

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      601 TAAAGTATCACCAGAGGGTGCTGTA 625
Db      1 TAAAGTACCACCAGAGGGTGCTCTA 25

RESULT 116
US-09-396-196F-126548
; Sequence 126548, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126548

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      634 TTGATATTACCATGGTGACGGCGT 658
Db      1 TTGATATTACCATGGCGATGGCGT 25

RESULT 117
US-09-396-196F-126549
; Sequence 126549, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126549

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      637 ATATTACCATGGTGACGGCGGTGGA 661
Db      1 ATATTACCATGGCGGATGGCGGTGGA 25

RESULT 118
US-09-396-196F-126551
; Sequence 126551, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126551

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      640 TTCACCATGGTGACGGCGGTGGAAGA 664
Db      1 TTCACCATGGCGGATGGCGGTGGAAGA 25

RESULT 119
US-09-396-196F-126552
; Sequence 126552, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126552

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      547 AGGCATCTGGCTTCTGTACGTCAA 571
Db      1 AAGCATCCGGCTTCTGTACGTCAA 25

RESULT 120
US-09-396-196F-126554
; Sequence 126554, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
```

```
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126554

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      553 CTGGCTTCTGTACGTCAATGATAT 577
Db      1 CCGGCTTCTGTACGTCAATGACAT 25

RESULT 121
US-09-396-196G-126545
; Sequence 126545, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126545

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      601 TAAAGTATCACCAGAGGGTGCTGTA 625
Db      1 TAAAGTACCACCAGAGGGTGCTCTA 25

RESULT 122
US-09-396-196G-126548
; Sequence 126548, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 126548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126548

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      634 TTGATATTACCATGGTGACGGCGT 658
Db      1 TTGATATTACCATGGCGATGGCGCT 25

RESULT 123
US-09-396-196G-126549
; Sequence 126549, Application US/093996196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126549

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      637 ATATTACCATGGTGACGGCGTGGA 661
Db      1 ATATTACCATGGCGATGGCGTGGA 25

RESULT 124
US-09-396-196G-126551
; Sequence 126551, Application US/093996196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126551

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      640 TTCACCATGGTGACGGCGTGAAGA 664
Db      1 TTCACCATGGCGATGGCGTGAAGA 25

RESULT 125
US-09-396-196G-126552
; Sequence 126552, Application US/093996196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126552

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      547 AGGCATCTGGCTTCTGTACGTCAA 571
Db      1 AAGCATCCGGCTTCTGTACGTCAA 25

RESULT 126
US-09-396-196G-126554
; Sequence 126554, Application US/093996196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126554

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      553 CTGGCTTCTGTACGTCAATGATAT 577
Db      1 CCGGCTTCTGTACGTCAATGACAT 25

RESULT 127
US-10-719-956-181943
; Sequence 181943, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
```

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; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-181943

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCAATGAT 575
Db 1 ATCCGGCTTCTGTACGTCAATGAT 25

RESULT 128
US-10-719-956-324416
; Sequence 324416, Application US/10/719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-324416

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCCGTGAATTGGGCT 518
Db 1 GACGGACATCGCCGTGAATTGGGCT 25

RESULT 129
US-10-719-956-324417
; Sequence 324417, Application US/10/719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-324417

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCCGTGAATTGGGCT 518
Db 1 GACGGACATCGCCGTGAATTGGGCT 25

RESULT 130
US-10-719-956-337746
; Sequence 337746, Application US/10/719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 337746
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-337746

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 GAGATGACCAAGTACCACGCGATG 321
Db 1 GAGATGACCAAGTACCACGCGACG 25

RESULT 131
US-10-719-956-417655
; Sequence 417655, Application US/10/719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417655

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 659 GGAAGAGCGCTTCTACACCGGAC 683
Db 1 GGAAGAGCGCTTCTATACCACGAC 25

RESULT 132
US-60-427-836-181943
; Sequence 181943, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181943
; LENGTH: 25

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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-181943

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCAATGAT 575
Db 1 ATCCGGCTTCTGTATACGTCAATGAT 25
      ||| ||||| ||||| ||||| |||||
      ||| ||||| ||||| ||||| |||||

RESULT 133
US-60-427-836-324416
; Sequence 324416, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-324416

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCCGTGAATTGGGCT 518
Db 1 GACGGACATCGCAGTGAACCTGGGCT 25
      ||||| ||||| ||||| ||||| |||||
      ||||| ||||| ||||| ||||| |||||

RESULT 134
US-60-427-836-324417
; Sequence 324417, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-324417

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCCGTGAATTGGGCT 518
Db 1 GACGGACATCGCAGTGAACCTGGGCT 25
      ||||| ||||| ||||| ||||| |||||
      ||||| ||||| ||||| ||||| |||||

RESULT 135
US-60-427-836-337746
; Sequence 337746, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836

```

US-60-507-481-100331/c
; Sequence 100331, Application US/60507481
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODLES OF INFLAMMATORY DISEASES
; FILE REFERENCE: AM101084
; CURRENT APPLICATION NUMBER: US/60/507,481
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 210107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-60-507-481-100331

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTGAGAAC 57
Db 25 TCTCCCACTCGGTCATCCTGAGAAC 1

RESULT 139
US-60-507-511-67531/c
; Sequence 67531, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-67531

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 TCAGCGRCTCTGTCACTCGGGGTAG 88
Db 25 TCAGCGTCTCTGTCACTCGGGGTAG 1

RESULT 140
US-60-507-511-79042
; Sequence 79042, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-79042

US-60-507-511-79043
; Sequence 79043, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-79043

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1036 CCCGGTGTGGACATATGAGACAGC 1060
Db 1 CCCGCTGCTGGACATATGAGACATC 25

RESULT 141
US-60-507-511-79043
; Sequence 79043, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-79043

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1036 CCCGGTGTGGACATATGAGACAGC 1060
Db 1 CCCGCTGCTGGACATATGAGACATC 25

RESULT 142
US-60-507-511-111888
; Sequence 111888, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-111888

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 630 GACATTGATATTCACCATGTTGACG 654
Db 1 GACATTGACATCCACCATGTTGACG 25

RESULT 143
US-60-507-511-111889
; Sequence 111889, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

```
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: AM 101081
/ CURRENT APPLICATION NUMBER: US/60/507,511
/ CURRENT FILING DATE: 2003-10-02
/ NUMBER OF SEQ ID NOS: 203623
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 111889
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-507-511-111889

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      630 GACATTGATATTCCACCATGGTGACG 654
Db      1 GACATTGACATCCACCATGGTGACG 25

RESULT 144
US-60-507-511-147894/c
; Sequence 147894, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-147894

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      67 GCGRCTCTGTCACCTCGGGGTAGACC 91
Db      25 GCGTCTCTGTCACCTCGGGGTAGACC 1

RESULT 145
US-09-420-692A-89/c
; Sequence 89, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-89

Query Match      1.4%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      138 AAAGTCTGTCTACTACTACGACGG 160
Db      23 AAAGTCTGTCTACTACTACGACGG 1
```

```
Best Local Similarity 92.0%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      212 AATCCGCATGACTCATAATTGCTG 236
Db      25 AATCCGCATGACCCCAACTTGCTG 1

RESULT 146
US-10-145-493B-89/c
; Sequence 89, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-89

Query Match      1.4%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      212 AATCCGCATGACTCATAATTGCTG 236
Db      25 AATCCGCATGACCCCAACTTGCTG 1

RESULT 147
US-09-420-692A-53/c
; Sequence 53, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-53

Query Match      1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      138 AAAGTCTGTCTACTACTACGACGG 160
Db      23 AAAGTCTGTCTACTACTACGACGG 1
```

RESULT 148
US-10-145-493B-53/c
; Sequence 53, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-53

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 AAAGTCGTCTACTACTACGACGG 160
Db 23 AAAGTCGTCTACTACTACGACGG 1

RESULT 149
US-10-310-188-30105
; Sequence 30105, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30105
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-30105

Query Match 1.3%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 61 GCCTGAGCGRCTCTGTCACTCGG 83
Db 1 GCCTGAGCGTCTCTGTCACTCGG 23

RESULT 150
US-10-154-659-16/c
; Sequence 16, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; TITLE OF INVENTION: genes regulated by trapoxin-induced HDAC inhibition
; FILE REFERENCE: 4-32017A

; CURRENT APPLICATION NUMBER: US/10/154,659
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-154-659-16

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1340 TGACAAACGAATTGCCTGTGA 1360
Db 21 TGACAAACGAATTGCCTGTGA 1

RESULT 151
US-09-420-692A-54/c
; Sequence 54, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 166 TTGGAAATTACTATTATGGACA 187
Db 22 TTGGAAATTATTATTATGGACA 1

RESULT 152
US-10-145-493B-54/c
; Sequence 54, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTAATTACTATTATGGACA 187
Db 22 TTGGAATTAATTACTATTATGGACA 1

RESULT 153
US-60-507-511-69977
; Sequence 69977, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-69977

Query Match 1.3%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 GGGTGCTGTACATTGACATTGA 637
Db 4 GGGTGCTGTACATTGACATTGA 25

RESULT 154
US-09-396-196F-126539
; Sequence 126539, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126539

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; APPLICANT: Michael Mittmann
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
US-09-396-196F-126550
; Sequence 126550, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

QY 541 AGTCCGAGGCATCTGGCTTCTGTTA 565
Db 1 AGTCTGAAGCATCCGGCTTCTGTTA 25

RESULT 155
US-09-396-196F-126546
; Sequence 126546, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126546

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 604 AGTATCACCAGAGGGTGTCTGTACAT 628
Db 1 AGTATCACCAGAGGGTGTCTGTATAT 25

RESULT 156
US-09-396-196F-126547
; Sequence 126547, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126547

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 607 ATCACCAGAGGGTGTCTGTACATTGA 631
Db 1 ACCACCAGAGGGTGTCTGTATATTGA 25

RESULT 157
US-09-396-196F-126550
; Sequence 126550, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann


```

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126550

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      544 CCGAGGCATCGGCTTCTGTACGT 568
      ||| ||||| ||||| ||||| |||||
Db      1 CTGAAGCATCCGGCTTCTGTACGT 25

RESULT 158
US-09-396-196G-126539
; Sequence 126539, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126539

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      541 AGTCCGAGGCATCTGGCTTCTGTGA 565
      ||||| ||||| ||||| ||||| |||||
Db      1 AGTCTGAAGCATCCGGCTTCTGTGA 25

RESULT 159
US-09-396-196G-126546
; Sequence 126546, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126546

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      604 AGTATCACCAGAGGGTGTGTACAT 628
      ||||| ||||| ||||| ||||| |||||
Db      1 AGTACCACAGAGGGTGTCTCTATAT 25

RESULT 160
US-09-396-196G-126547
; Sequence 126547, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126547

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      607 ATCACCAGAGGGTGTGTACATTGA 631
      ||||| ||||| ||||| ||||| |||||
Db      1 ACCACCAGAGGGTGTCTCTATATTGA 25

RESULT 161
US-09-396-196G-126550
; Sequence 126550, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126550

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      544 CCGAGGCATCTGGCTTCTGTACGT 568
```



```
RESULT 167
US-10-719-956-319560
; Sequence 319560, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-319560

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      630 GACATTGATATTCACCATGGTGACG 654
      |||||
Db      1 GACATTGACATTCACCATGGCGATG 25

RESULT 168
US-10-719-956-356287
; Sequence 356287, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-356287

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      432 GAGTCTGTGTCAGTTGTCTACTGGTG 456
      |||||
Db      1 GAGTCTGTGTCAGTTGTCTCCATGGGTG 25

RESULT 169
US-10-719-956-417657
; Sequence 417657, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
```

```
US-10-719-956-417657

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      659 GGAAGAGGCGCTTCTACACCGGAC 683
      |||||
Db      1 GGAAGAGGCGCTTGTATACACAGAC 25

RESULT 170
US-10-719-956-444838
; Sequence 444838, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-444838

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      456 GGTCTGTGGCAAGTGTCTGAAAC 480
      |||||
Db      1 GGCTCTGTGCGAGTGTCTGAAAC 25

RESULT 171
US-60-233-166-71840/c
; Sequence 71840, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819408
US-60-233-166-71840

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1342 ACAACGAATTCCTGTGAGGAAGA 1366
      |||||
Db      25 ACAACGAATTCCTGTGAGGAAGA 1

RESULT 172
US-60-427-836-140528
; Sequence 140528, Application US/60427836
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 140528
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-140528
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      403 AGGACTGTCCAGTATTTCGATGGCCT 427
      |||||
Db      1 AGGACTGTCCGGTATTTCGATGGCCT 25
```

```
RESULT 173
US-60-427-836-319560
; Sequence 319560, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-319560
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      630 GACATTGATATTACCATGGTGACG 654
      |||||
Db      1 GACATTGACATTCACCATGGCGATG 25
```

```
RESULT 174
US-60-427-836-356287
; Sequence 356287, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-356287
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      432 GAGTTCTGTCAGTTGCTACTGGTG 456
      |||||
Db      1 GAGTTCTGTCAGTTGCTCCATGGTG 25
```

```
RESULT 175
US-60-427-836-417657
; Sequence 417657, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-417657
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      659 GGAAGAGGCCTTCTACACCCGAC 683
      |||||
Db      1 GGAAGAGGCCTTGTATACCCAGAC 25
```

```
RESULT 176
US-60-427-836-444838
; Sequence 444838, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-444838
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      456 GGTTCTGTGGCAAGTGCTGTGAAAC 480
      |||||
Db      1 GGCTCTGTGCGAGTGCTGTGAAAC 25
```

```
RESULT 177
US-60-507-511-178470
; Sequence 178470, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-178470
```

```
Query Match      1.3%; Score 20.2; DB 1; Length 25;
```

```
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 TCTACACGACGACCGGGTTCATGAC 694
    ||||| ||| ||||| ||||| |||||
Db 1 TCTACCTCACTGACCGGGTTCATGAC 25

RESULT 178
US-60-507-511-178471
; Sequence 178471, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-178471

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 TCTACACGACGACCGGGTTCATGAC 694
    ||||| ||| ||||| ||||| |||||
Db 1 TCTACCTCACTGACCGGGTTCATGAC 25

RESULT 179
PCT-US01-46518A-12/c
; Sequence 12, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGGAGCAAGATGGCGCAGA 120
    ||||| ||||| ||||| |||||
Db 20 GCGGAGCAAGATGGCGCAGA 1

RESULT 180
PCT-US01-46518A-13/c
; Sequence 13, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
```

```
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCTGTACTACT 153
    ||||| ||||| ||||| |||||
Db 20 GAGGAAAGTCTGTACTACT 1

RESULT 181
PCT-US01-46518A-14/c
; Sequence 14, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
    ||||| ||||| ||||| |||||
Db 20 AATTGCTGCTCAACTATGG 1

RESULT 182
PCT-US01-46518A-15/c
; Sequence 15, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
```



```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-15

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 GCTGCTCAACTATGGTCTCT 252
      |||||
Db 20 GCTGCTCAACTATGGTCTCT 1

RESULT 183
PCT-US01-46518A-16/c
; Sequence 16, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-16

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGGTCTCTACCGA 257
      |||||
Db 20 TCAACTATGGTCTCTACCGA 1

RESULT 184
PCT-US01-46518A-17/c
; Sequence 17, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-17

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGGTCTCTACCGAAAAAT 262
      |||||
Db 20 TATGGTCTCTACCGAAAAAT 1

RESULT 185
PCT-US01-46518A-18/c
; Sequence 18, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-18

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCCTCACAAGCCCAATGC 292
      |||||
Db 20 CGCCCTCACAAGCCCAATGC 1

RESULT 186
PCT-US01-46518A-19/c
; Sequence 19, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-19

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCCAATGCTGAGG 297
      |||||
Db 20 TCACAAAGCCCAATGCTGAGG 1

RESULT 187
PCT-US01-46518A-20/c
; Sequence 20, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
```

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; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-20

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      283 AAGCCAATGCTGAGGAGATG 302
Db      20 AAGCCAATGCTGAGGAGATG 1

RESULT 188
PCT-US01-46518A-21/c
; Sequence 21, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-21

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      288 AATGCTGAGGAGATGACCAA 307
Db      20 AATGCTGAGGAGATGACCAA 1

RESULT 189
PCT-US01-46518A-22/c
; Sequence 22, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

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; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-22

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      293 TGAGGAGATGACCAAGTACC 312
Db      20 TGAGGAGATGACCAAGTACC 1

RESULT 190
PCT-US01-46518A-23/c
; Sequence 23, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-23

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      369 TACAGCAAGCAGATGCACAG 388
Db      20 TACAGCAAGCAGATGCACAG 1

RESULT 191
PCT-US01-46518A-24/c
; Sequence 24, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-24

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      405 GACTGTCCAGTATTCGATGG 424
Db      20 GACTGTCCAGTATTCGATGG 1
```

```
RESULT 192
PCT-US01-46518A-25/c
; Sequence 25, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-25

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 TGTTCAGTTCTGTGTCAGTTG 446
      |||||||
Db 20 TGTTCAGTTCTGTGTCAGTTG 1

RESULT 193
PCT-US01-46518A-26/c
; Sequence 26, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-26

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 TGTTCAGTTCTGTGTCAGTTG 446
      |||||||
Db 20 TGTTCAGTTCTGTGTCAGTTG 1

RESULT 194
PCT-US01-46518A-27/c
; Sequence 27, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
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```
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-27

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGCGGACATCG 504
      |||||||
Db 20 TAAGCAGCAGCGGACATCG 1

RESULT 195
PCT-US01-46518A-29/c
; Sequence 29, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-29

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 ATCGTCTTGCCCATCCTGGA 595
      |||||||
Db 20 ATCGTCTTGCCCATCCTGGA 1

RESULT 196
PCT-US01-46518A-30/c
; Sequence 30, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-30
```

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGGCCATCCTGGAACGTC 600
Db 20 CTTGGCCATCCTGGAACGTC 1

RESULT 197
PCT-US01-46518A-31/c
; Sequence 31, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-31

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GCGTGGAAGAGGCCTTCTA 673
Db 20 GCGTGGAAGAGGCCTTCTA 1

RESULT 198
PCT-US01-46518A-32/c
; Sequence 32, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-32

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 GAGGCCTTCTACACCGGA 682
Db 20 GAGGCCTTCTACACCGGA 1

RESULT 199

PCT-US01-46518A-33/c
; Sequence 33, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-33

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 GGAGAGTACTTCCCAGGAAC 733
Db 20 GGAGAGTACTTCCCAGGAAC 1

RESULT 200
PCT-US01-46518A-34/c
; Sequence 34, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-34

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCCAGGAAGTGGG 738
Db 20 GTACTTCCCAGGAAGTGGG 1

RESULT 201
PCT-US01-46518A-35/c
; Sequence 35, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167

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; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-35

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 TCCAGGAAGTGGGACCTA 743
Db 20 TCCAGGAAGTGGGACCTA 1

RESULT 202
PCT-US01-46518A-36/c
; Sequence 36, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-36

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 GGAAGTGGGACCTACGGGA 748
Db 20 GGAAGTGGGACCTACGGGA 1

RESULT 203
PCT-US01-46518A-37/c
; Sequence 37, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-37
```

Query Match 1.2%; Score 20; DB 1; Length 20;

```
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTTAACTAC 788
Db 20 AGTATTATGCTGTTAACTAC 1

RESULT 204
PCT-US01-46518A-38/c
; Sequence 38, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-38

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CCCGCTCCGAGACGGGATTG 807
Db 20 CCCGCTCCGAGACGGGATTG 1

RESULT 205
PCT-US01-46518A-39/c
; Sequence 39, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-39

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACAGTCCTATGAGGCCATT 830
Db 20 ACAGTCCTATGAGGCCATT 1

RESULT 206
PCT-US01-46518A-40/c
; Sequence 40, Application PC/TUS0146518A
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; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-40

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      840 GTCATGTCCAAAGTAATGGA 859
Db      20 GTCATGTCCAAAGTAATGGA 1

RESULT 207
PCT-US01-46518A-41/c
; Sequence 41, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      845 GTCCAAAGTAATCGAGATGT 864
Db      20 GTCCAAAGTAATCGAGATGT 1

RESULT 208
PCT-US01-46518A-42/c
; Sequence 42, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
```

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; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      850 AAGTAATGGAGATGTTCCAG 869
Db      20 AAGTAATGGAGATGTTCCAG 1

RESULT 209
PCT-US01-46518A-43/c
; Sequence 43, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      859 AGATGTTCCAGCCTAGTGC 878
Db      20 AGATGTTCCAGCCTAGTGC 1

RESULT 210
PCT-US01-46518A-44/c
; Sequence 44, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-44

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 905 CCTATCTGGGGATCGGTTAG 924
Db 20 CCTATCTGGGGATCGGTTAG 1

RESULT 211
PCT-US01-46518A-45/c
; Sequence 45, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-45

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGGTTAGGTTGCTTCAATCT 937
Db 20 CGGTTAGGTTGCTTCAATCT 1

RESULT 212
PCT-US01-46518A-46/c
; Sequence 46, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-46

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 ATCAAAGGACACGCCAAGTG 961
Db 20 ATCAAAGGACACGCCAAGTG 1

RESULT 213
PCT-US01-46518A-47/c
; Sequence 47, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-47

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 947 AGGACACGCCCAAGTGTGTGG 966
Db 20 AGGACACGCCCAAGTGTGTGG 1

RESULT 214
PCT-US01-46518A-48/c
; Sequence 48, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-48

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 GAGGCGGTGTTACACCAT 1025
Db 20 GAGGCGGTGTTACACCAT 1

RESULT 215
PCT-US01-46518A-49/c
; Sequence 49, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 49
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-49

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGGCCCTGGATAC 1075
Db 20 ACAGCTGTGGCCCTGGATAC 1

RESULT 216
PCT-US01-46518A-50/c
; Sequence 50, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-50

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 ACAATGACTACTTTGAATAC 1118
Db 20 ACAATGACTACTTTGAATAC 1

RESULT 217
PCT-US01-46518A-51/c
; Sequence 51, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-51

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1172 CACGAATGAGTACTGGAGA 1191

Db 20 CACGATGAGTACTGGAGA 1

RESULT 218
PCT-US01-46518A-52/c
; Sequence 52, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-52

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAAGATCAA 1198
Db 20 GAGTACCTGGAGAAGATCAA 1

RESULT 219
PCT-US01-46518A-54/c
; Sequence 54, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-54

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAAGACGACCCCTGAC 1316
Db 20 AGGACGAAGACGACCCCTGAC 1

RESULT 220
PCT-US01-46518A-55/c
; Sequence 55, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.

; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCCTGACAAGCGCATCTC 1327
Db 20 GACCCTGACAAGCGCATCTC 1

RESULT 221

PCT-US01-46518A-56/c
; Sequence 56, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-56

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCCTGTGAGGAAGAGTT 1369
Db 20 ATTGCCTGTGAGGAAGAGTT 1

RESULT 222

PCT-US01-46518A-57/c
; Sequence 57, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-57

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGAAGAGGAGGAGGAGGGG 1397
Db 20 CTGAAGAGGAGGAGGAGGGG 1

RESULT 223

PCT-US01-46518A-58/c
; Sequence 58, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-58

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAAGAGAAAGACCC 1468
Db 20 GATGAAAAAGAGAAAGACCC 1

RESULT 224

PCT-US01-46518A-59/c
; Sequence 59, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-59

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAAACCAAGGAGGAGAGC 1518
Db 20 GAAAACCAAGGAGGAGAGC 1

```
RESULT 225
PCT-US01-46518A-60/c
; Sequence 60, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-60

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 226
PCT-US01-46518A-61/c
; Sequence 61, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-61

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GAGGAGAGCCAGAGCCAA 1528
Db 20 GAGGAGAGCCAGAGCCAA 1

RESULT 227
PCT-US01-46518A-62/c
; Sequence 62, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
```

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; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-62

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAAGCCAGAGCCAAAGGG 1533
Db 20 GAAGCCAGAGCCAAAGGG 1

RESULT 228
PCT-US01-46518A-63/c
; Sequence 63, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-63

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTGGCCTGAATGGACCT 1567
Db 20 AAGTGGCCTGAATGGACCT 1

RESULT 229
PCT-US01-46518A-64/c
; Sequence 64, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```


PCT-US01-46518A-64

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTGGCTTC 1584
Db 20 CCTCTCCAGCTCTGGCTTC 1

RESULT 230
US-09-420-692A-35/c
; Sequence 35, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-35

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 CCCGCTGGTGTCTGTCTC 36
Db 20 CCCGCTGGTGTCTGTCTC 1

RESULT 231
US-09-420-692A-36/c
; Sequence 36, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-36

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GCTGTCTCCACTCGGTTCAT 48
Db 20 GCTGTCTCCACTCGGTTCAT 1

RESULT 232
US-09-420-692A-37/c
; Sequence 37, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-37

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 TGTCTCCCACTCGGTTCATCC 50
Db 20 TGTCTCCCACTCGGTTCATCC 1

RESULT 233
US-09-420-692A-38/c
; Sequence 38, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-38

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 TCTCCCACTCGGTTCATCTG 52
Db 20 TCTCCCACTCGGTTCATCTG 1

RESULT 234
US-09-420-692A-39/c
; Sequence 39, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William

```

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTGAGAACACA 60
Db 20 TCGGTCATCCTGAGAACACA 1

RESULT 235
US-09-420-692A-41/c
; Sequence 41, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 236
US-09-420-692A-43/c
; Sequence 43, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-41
```

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 237
US-09-420-692A-44/c
; Sequence 44, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-44

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 238
US-09-563-728A-1/c
; Sequence 1, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-728A-1

Query Match      1.2%; Score 20; DB 1; Length 20;
```

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604
|||||
Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 239
US-09-563-728A-10/c
; Sequence 10, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-10

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604
|||||
Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 240
US-09-754-167-12/c
; Sequence 12, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGAGCACAGATGGCGCAGA 120
|||||
Db 20 GCGAGCACAGATGGCGCAGA 1

RESULT 241

US-09-754-167-13/c
; Sequence 13, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCTGTTACTACT 153
|||||
Db 20 GAGGAAAGTCTGTTACTACT 1

RESULT 242
US-09-754-167-14/c
; Sequence 14, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
|||||
Db 20 AATTGCTGCTCAACTATGG 1

RESULT 243
US-09-754-167-15/c
; Sequence 15, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-15

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 GCTGCTCAACTATGGTCTCT 252
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCTGCTCAACTATGGTCTCT 1

RESULT 244
US-09-754-167-16/c
; Sequence 16, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-16

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGGTCTCTACCGA 257
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TCAACTATGGTCTCTACCGA 1

RESULT 245
US-09-754-167-17/c
; Sequence 17, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGGTCTCTACCGAAAAAT 262
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TATGGTCTCTACCGAAAAAT 1

RESULT 246
US-09-754-167-18/c
; Sequence 18, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION

FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 18
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCCTCACAAAGCCAATGC 292
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CGCCCTCACAAAGCCAATGC 1

RESULT 247
US-09-754-167-19/c
; Sequence 19, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-19

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCAATGCTGAGG 297
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TCACAAAGCCAATGCTGAGG 1

RESULT 248
US-09-754-167-20/c
; Sequence 20, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-20

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AAGCCAATGCTGAGGAGATG 302

```
Db      20  AAGCCAATGCTGAGGAGATG 1
|||||
RESULT 249
US-09-754-167-21/c
; Sequence 21, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-21
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      288  AATGCTCAGGAGATGACCAA 307
|||||
Db      20  AATGCTCAGGAGATGACCAA 1
|||||
RESULT 250
US-09-754-167-22/c
; Sequence 22, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-22
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      293  TGAGGAGATGACCAAGTACC 312
|||||
Db      20  TGAGGAGATGACCAAGTACC 1
|||||
RESULT 251
US-09-754-167-23/c
; Sequence 23, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-23
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      405  GACTGTCCAGTATTCGATGG 424
|||||
Db      20  GACTGTCCAGTATTCGATGG 1
|||||
RESULT 253
US-09-754-167-25/c
; Sequence 25, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-25
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      427  TGTTCAGTTCGTCTGTCAGTTG 446
|||||
Db      20  TGTTCAGTTCGTCTGTCAGTTG 1
|||||
RESULT 254
US-09-754-167-26/c
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-26
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      427  TGTTCAGTTCGTCTGTCAGTTG 446
|||||
Db      20  TGTTCAGTTCGTCTGTCAGTTG 1
|||||
RESULT 254
US-09-754-167-26/c
```


; Sequence 26, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-26

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 CTTAATAAGCAGCAGACGGA 499
Db 20 CTTAATAAGCAGCAGACGGA 1

RESULT 255

US-09-754-167-27/c
; Sequence 27, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-27

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGCAGACATCG 504
Db 20 TAAGCAGCAGCAGACATCG 1

RESULT 256

US-09-754-167-29/c
; Sequence 29, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-29

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 576 ATCGTCTTGGCCATCCTGGA 595
Db 20 ATCGTCTTGGCCATCCTGGA 1

RESULT 257

US-09-754-167-30/c
; Sequence 30, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-30

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGGCCATCCTGGAATGC 600
Db 20 CTTGGCCATCCTGGAATGC 1

RESULT 258

US-09-754-167-31/c
; Sequence 31, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-31

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GCGGTGAAGAGGCGCTTCTA 673
Db 20 GCGGTGAAGAGGCGCTTCTA 1

RESULT 259

US-09-754-167-32/c
; Sequence 32, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140

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; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-32

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      663 GAGGCCTTCTACACACGGA 682
Db      20 GAGGCCTTCTACACACGGA 1

RESULT 260
US-09-754-167-33/c
; Sequence 33, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      724 TCCAGGAAGTGGGACCTA 743
Db      20 TCCAGGAAGTGGGACCTA 1

RESULT 263
US-09-754-167-36/c
; Sequence 36, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-36

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      729 GGAAGTGGGACCTACGGGA 748
Db      20 GGAAGTGGGACCTACGGGA 1

RESULT 264
US-09-754-167-37/c
; Sequence 37, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      714 GGAGAGTACTTCCAGGAAC 733
Db      20 GGAGAGTACTTCCAGGAAC 1

RESULT 261
US-09-754-167-34/c
; Sequence 34, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-34

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      719 GTACTTCCAGGAAGTGGG 738
Db      20 GTACTTCCAGGAAGTGGG 1
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTTAACTAC 788
    |||||
Db 20 AGTATTATGCTGTTAACTAC 1

RESULT 265
US-09-754-167-38/c
; Sequence 38, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CCCGCTCCGAGACGGGATTG 807
    |||||
Db 20 CCCGCTCCGAGACGGGATTG 1

RESULT 266
US-09-754-167-39/c
; Sequence 39, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCCTATGAGGCCATT 830
    |||||
Db 20 ACGAGTCCTATGAGGCCATT 1

RESULT 267
US-09-754-167-40/c
; Sequence 40, Application US/09754167

; ORGANISM: Artificial Sequence
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-40

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GTCATGTCCAAAGTAATGGA 859
    |||||
Db 20 GTCATGTCCAAAGTAATGGA 1

RESULT 268
US-09-754-167-41/c
; Sequence 41, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 GTCCAAAGTAATGGAGATGT 864
    |||||
Db 20 GTCCAAAGTAATGGAGATGT 1

RESULT 269
US-09-754-167-42/c
; Sequence 42, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

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```

US-09-754-167-45

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      918  CGGTTAGGTGCTTCAATCT 937
          |||||
Db       20  CGGTTAGGTGCTTCAATCT 1

```

; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION

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; CURRENT APPLICATION NUMBER: US/09/754,167
;
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
;

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;
; LENGTH: 20
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;

```

```

US-09-754-167-46

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      942 ATCAAAGGACACGCCAAGTG 961
      |||||
Db      20 ATCAAAGGACACGCCAAGTG 1

```

US 03-054167 A1
; Sequence 47, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION

```

;
; CURRENT APPLICATION NUMBER: US/09/754,167
;
; CURRENT FILING DATE: 2000-12-19
;
; NUMBER OF SEQ ID NOS: 87
;
; SEQ ID NO 47
;
; LENGTH: 20
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;

```

```
US-09-754-167-47
```

	Query Match	1.2%;	Score 20;	DB 1;	Length 20;
	Best Local Similarity	100.0%;	Pred. No.	1.1e+02;	
	Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Oy	947	AGGACACGCCCAAGTGTGG	966		
Dd	20	AGGACACGCCCAAGTGTGG	1		

Query Match	1.2%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.1e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	947	AGGACACGCCCAAGTGTGTGG	966	
Db	20	AGGACACGCCCAAGTGTGTGG	1	

```
RESULT 275
US-09-754-167-48/c
; Sequence 48, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-48

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 GAGCGGTGGTTACACCAT 1025
   |||||
Db 20 GAGCGGTGGTTACACCAT 1

RESULT 276
US-09-754-167-49/c
; Sequence 49, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-49

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 GAGCGGTGGTTACACCAT 1025
   |||||
Db 20 GAGCGGTGGTTACACCAT 1

RESULT 277
US-09-754-167-50/c
; Sequence 50, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-50

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 ACAATGACTACTTGAATAC 1118
   |||||
Db 20 ACAATGACTACTTGAATAC 1

RESULT 278
US-09-754-167-51/c
; Sequence 51, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-51

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1172 CACGAATGAGTACCTGGAGA 1191
   |||||
Db 20 CACGAATGAGTACCTGGAGA 1

RESULT 279
US-09-754-167-52/c
; Sequence 52, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-52

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAAGATCAA 1198
   |||||
Db 20 GAGTACCTGGAGAAGATCAA 1

RESULT 280
US-09-754-167-54/c
; Sequence 54, Application US/09754167
; GENERAL INFORMATION:
```


APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 54
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-54

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAAGACGACCCCTGAC 1316
Db 20 AGGACGAAGACGACCCCTGAC 1

RESULT 281
US-09-754-167-55/c
Sequence 55, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 55
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCCTGACAAGCGCATCTC 1327
Db 20 GACCCTGACAAGCGCATCTC 1

RESULT 282
US-09-754-167-56/c
Sequence 56, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-56

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCCTGACAAGCGCATCTC 1327
Db 20 GACCCTGACAAGCGCATCTC 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCCTGTGAGGAAGAGTT 1369
Db 20 ATTGCCTGTGAGGAAGAGTT 1

RESULT 283
US-09-754-167-57/c
Sequence 57, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 57
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-57

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGAAGAGGAGGAGAGGGG 1397
Db 20 CTGAAGAGGAGGAGAGGGG 1

RESULT 284
US-09-754-167-58/c
Sequence 58, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-58

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAAGAGAAAGACCC 1468
Db 20 GATGAAAAAGAGAAAGACCC 1

RESULT 285
US-09-754-167-59/c
Sequence 59, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19

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; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-59

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAACCAAGGAGGAGGAGC 1518
Db 20 GAAACCAAGGAGGAGGAGC 1

RESULT 286
US-09-754-167-60/c
; Sequence 60, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-60

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 287
US-09-754-167-61/c
; Sequence 61, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-61

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GAGGAGAGCCAGAGCCAA 1528
Db 20 GAGGAGAGCCAGAGCCAA 1

RESULT 288
US-09-754-167-62/c
; Sequence 62, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-62

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAAGCCAGAGCCAAAGGG 1533
Db 20 GAAGCCAGAGCCAAAGGG 1

RESULT 289
US-09-754-167-63/c
; Sequence 63, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-63

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGGCCTGAATGGACCT 1567
Db 20 AAGTTGGCCTGAATGGACCT 1

RESULT 290
US-09-754-167-64/c
; Sequence 64, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-64

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
Db      20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 291
US-09-817-538-17/c
; Sequence 17, Application US/09817538
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 292
US-09-817-538-18/c
; Sequence 18, Application US/09817538
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 293
US-09-817-913-17/c
; Sequence 17, Application US/09817913
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 294
US-09-817-913-18/c
; Sequence 18, Application US/09817913
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
Db      20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 295
US-10-051-819B-1/c
; Sequence 1, Application US/10051819B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-64

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
Db      20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 291
US-09-817-538-17/c
; Sequence 17, Application US/09817538
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 292
US-09-817-538-18/c
; Sequence 18, Application US/09817538
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 293
US-09-817-913-17/c
; Sequence 17, Application US/09817913
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCAGTTTC 1604
Db      20 TGCTGAGTCCCTCAGTTTC 1

RESULT 294
US-09-817-913-18/c
; Sequence 18, Application US/09817913
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
Db      20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 295
US-10-051-819B-1/c
; Sequence 1, Application US/10051819B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
```

; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
DB 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 296
US-10-051-819B-2/c
; Sequence 2, Application US/10051819B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-2

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
DB 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 297
US-10-052-390B-1/c
; Sequence 1, Application US/10052390B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B

; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
DB 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 298
US-10-052-390B-2/c
; Sequence 2, Application US/10052390B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
DB 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 299
US-10-145-493B-35/c
; Sequence 35, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 35

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-35

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTCTGCTGCTC 36
Db 20 CCCGCTGGTCTGCTGCTC 1

RESULT 300
US-10-145-493B-36/c
; Sequence 36, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-36

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCCACTCGGTGTCAT 48
Db 20 GCTGTCTCCCACTCGGTGTCAT 1

RESULT 301
US-10-145-493B-37/c
; Sequence 37, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer

```

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US-10-145-493B-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCCACTCGGTGTCATCC 50
Db 20 TGTCTCCCACTCGGTGTCATCC 1

RESULT 302
US-10-145-493B-38/c
; Sequence 38, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCCTCCCACTCGGTGTCATCCTG 52
Db 20 TCCTCCCACTCGGTGTCATCCTG 1

RESULT 303
US-10-145-493B-39/c
; Sequence 39, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


[illegible]

RESULT 308
US-10-189-818B-8/c
; Sequence 8, Application US/10189818B
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-8

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGCTTTC 1604
|||||
Db 20 TGCTGAGTCCCTCAGCTTTC 1

RESULT 309
US-10-189-818B-10/c
; Sequence 10, Application US/10189818B
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-10

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 310
US-10-751-736-43855/c
; Sequence 43855, Application US/10751736

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43855
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-43855

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 131 CCGAGAGAAAGTCTGTACTA 151
|||||
Db 21 CCGAGAGAAAGTCTGTACTA 1

RESULT 311
US-09-458-813-25/c
; Sequence 25, Application US/09458813
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT LIVE-ATTENUATED PARAINFLUENZA VIRUS
; TITLE OF INVENTION: (PIV) AS A VECTOR TO PROTECT AGAINST DISEASE CAUSED BY
; TITLE OF INVENTION: PIV AND RESPIRATORY SYNCYTIAL VIRUS (RSV)
; FILE REFERENCE: 17634-000330
; CURRENT APPLICATION NUMBER: US/09/458,813
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 09/083,793
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/047,575
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/059,385
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: insert to conform inserted sequence to rule of
; OTHER INFORMATION: six.
US-09-458-813-25

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTGATATTCACCATGGTGACGGC 656
|||||
Db 24 ATTGCTATTCACCATGCAGACGGC 1

RESULT 312
US-09-459-062-18/c

; Sequence 18, Application US/09459062
; GENERAL INFORMATION:
; APPLICANT: Tao, Tao
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; TITLE OF INVENTION: CONSTRUCTION AND USE OF RECOMBINANT PARAINFLUENZA
; TITLE OF INVENTION: VIRUSES EXPRESSING A CHIMERIC GLYCOPROTEIN
; FILE REFERENCE: 17634-00034CUS
; CURRENT APPLICATION NUMBER: US/09/459,062
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 09/083,793
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/059,385
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/047,575
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
; OTHER INFORMATION: primer.
US-09-459-062-18

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 633 ATTGATATTACCATGGTGACGGC 656
Db 24 ATTGCTATTACCATGCAGACGGC 1

RESULT 313
US-09-733-692A-24/c
; Sequence 24, Application US/09733692A
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
; OTHER INFORMATION: primer
US-09-733-692A-24

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 633 ATTGATATTACCATGGTGACGGC 656
Db 24 ATTGCTATTACCATGCAGACGGC 1

RESULT 314
PCT-US01-46518A-28/c
; Sequence 28, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-28

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 490 AGCAGACGACATCGCCGTG 509
Db 20 AGCAGACGACATCGCTGTG 1

RESULT 315
PCT-US01-46518A-53/c
; Sequence 53, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-53

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1246 TCCAAACGACGCGATTCCT 1265
Db 20 TCCAAATGCAGGCGATTCCT 1

RESULT 316
US-09-420-692A-40/c
; Sequence 40, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197

```
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-40

Query Match          1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGAGCGRCTCTGTCACTC 81
Db      20 CCTGAGCGTCTCTGTCACTC 1

RESULT 317
US-09-420-692A-42/c
; Sequence 42, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-42

Query Match          1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1531 GGGTCAAGGAGGAGGCCAAG 1550
Db      20 GGGTCAAGGAGGAGGTCAAG 1

RESULT 318
US-09-754-167-28/c
; Sequence 28, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-28

Query Match          1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGAGCGRCTCTGTCACTC 81
Db      20 CCTGAGCGTCTCTGTCACTC 1

RESULT 319
US-09-754-167-53/c
; Sequence 53, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-53

Query Match          1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1246 TCCAAACGCGAGCGGATTCCT 1265
Db      20 TCCAAATGCGAGCGGATTCCT 1

RESULT 320
US-10-145-493B-40/c
; Sequence 40, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-40

Query Match          1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGAGCGRCTCTGTCACTC 81
Db      20 CCTGAGCGTCTCTGTCACTC 1

RESULT 321
US-09-754-167-28
```

US-10-145-493B-42/c
 ; Sequence 42, Application US/10145493B
 ; GENERAL INFORMATION:
 ; APPLICANT: Besterman, Jeffrey
 ; APPLICANT: MacLeod, Robert
 ; APPLICANT: Siders, William
 ; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
 ; FILE REFERENCE: MET-015DV
 ; CURRENT APPLICATION NUMBER: US/10/145,493B
 ; CURRENT FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 09/420,692
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: US 60/104,804
 ; PRIOR FILING DATE: 1998-10-19
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 42
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 US-10-145-493B-42

Query Match 1.1%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAAGGAGGAGGCCAAG 1550
 |||||
 Db 20 GGGTCAAGGAGGAGGTCAAG 1

RESULT 322
 US-10-154-659-12/c
 ; Sequence 12, Application US/10154659
 ; GENERAL INFORMATION:
 ; APPLICANT: Buxton, Francis P.
 ; APPLICANT: Cohen, Dalia
 ; APPLICANT: Fischer, Denise D
 ; APPLICANT: Wang, Shaowen
 ; TITLE OF INVENTION: Antisense oligonucleotides directed to
 ; FILE REFERENCE: 4-32017A
 ; CURRENT APPLICATION NUMBER: US/10/154,659
 ; CURRENT FILING DATE: 2002-08-22
 ; PRIOR APPLICATION NUMBER: 60/293,090
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: 60/344,416
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: 60/370,332
 ; PRIOR FILING DATE: 2002-04-05
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antisense oligonucleotide
 ; NAME/KEY: modified_base
 ; LOCATION: (6)...(13)
 ; OTHER INFORMATION: 2'-H, phosphorothioate
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 2
 ; OTHER INFORMATION: 2' methoxyethyl 5-methyl cytidine
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 1,3-5, 14-18
 ; OTHER INFORMATION: 2'-O-methoxyethyl
 US-10-154-659-12

Query Match 1.1%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 AACATGTCGGAGTACAGC 374
 |||||
 Db 18 AACATGTCGGAGTACAGC 1

RESULT 323
 US-10-751-736-43856/c
 ; Sequence 43856, Application US/10751736
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Martinez, Robert
 ; APPLICANT: Brown, Eugene
 ; APPLICANT: Liu, Wei
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
 ; TITLE OF INVENTION: CANCERS
 ; FILE REFERENCE: AM100927 (031896-002000)
 ; CURRENT APPLICATION NUMBER: US/10/751,736
 ; CURRENT FILING DATE: 2003-01-06
 ; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
 ; PRIOR FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 54873
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 43856
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: RNAi
 US-10-751-736-43856

Query Match 1.1%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 ACCCGGAGGAAAGTCTGTAC 149
 |||||
 Db 21 AACCGGAGGAAAGTCTGTAC 1

RESULT 324
 US-10-266-090-51356/c
 ; Sequence 51356, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN
 ; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
 ; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
 ; FILE REFERENCE: NADII.058C1
 ; CURRENT APPLICATION NUMBER: US/10/266,090
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US 10/260,703
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/326,117
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 51812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 51356
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
 US-10-266-090-51356

Query Match 1.1%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1380 GAAGAGGAGGAGAGGGG 1398
Db 20 GAAGAGGAGAGAGAGGGG 2

RESULT 325
PCT-US98-04571A-122
; Sequence 122, Application PC/TUS9804571A
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: GENETIC COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 686
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04571A
; FILING DATE: 03-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,125
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 08/813,159
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-029002PC
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US98-04571A-122

Query Match 1.1%; Score 17; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1480 AAGGAATCACCAGAGGA 1498
Db 3 AAGGAACCCGAGAGGA 21

RESULT 326
US-08-813-159-122
; Sequence 122, Application US/08813159
; GENERAL INFORMATION:
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Chee, Mark
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Berno, Anthony
; TITLE OF INVENTION: Genetic Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,159
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-029001US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-813-159-122

Query Match 1.1%; Score 17; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1480 AAGGAATCACCAGAGGA 1498
Db 3 AAGGAACCCGAGAGGA 21

RESULT 327
PCT-US02-29148-65/c
; Sequence 65, Application PC/TUS0229148
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0413
; CURRENT APPLICATION NUMBER: PCT/US02/29148
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-29148-65

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGCCTGCACCATGCAA 537
Db 20 TGGGAGCCTGCACCAAGCAA 1

RESULT 328
US-09-514-000-14731


```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28225
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-28225

Query Match      1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1404 AAGAACTCTTCCAACTTCAA 1423
Db      2 AAGAACTCTTCCAACTTCAA 21

RESULT 334
US-10-751-736-28228
; Sequence 28228, Application US/10751736
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28228
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-28228

Query Match      1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1404 AAGAACTCTTCCAACTTCAA 1423
Db      1 AAGAACTCTTCCAACTTCAA 20

RESULT 335
PCT-US02-38147-198/c
; Sequence 198, Application PC/TUS0238147
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods

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; FILE REFERENCE: FP-IX 5532
; CURRENT APPLICATION NUMBER: PCT/US02/38147
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1453 AAAAAGAGAAAGACCCA 1469
Db      17 AAAAAGAGAAAGAYCCA 1

RESULT 336
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-995-529-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1453 AAAAAGAGAAAGACCCA 1469
Db      17 AAAAAGAGAAAGAYCCA 1

RESULT 337
US-10-011-250-198/c
; Sequence 198, Application US/10011250
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 5082
; CURRENT APPLICATION NUMBER: US/10/011,250
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

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; FEATURE:
; OTHER INFORMATION: Primer
US-10-011-250-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 338
US-10-310-188-43026
; Sequence 43026, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43026
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-43026

Query Match      1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1465 ACCCAGGAGAGAAAG 1482
Db 1 ACCCAGTGGAGAGAAAG 18

RESULT 339
PCT-US03-35845-27/c
; Sequence 27, Application PC/TUS0335845
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11 E
; FILE REFERENCE: ISIS0008-500WO (HTS-0090WO)
; CURRENT APPLICATION NUMBER: PCT/US03/35845
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/293,863
; PRIOR FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US03-35845-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1512 GAGAGCCAGAGCCAAA 1529
Db 19 GTGAGCCAGAGCCAAA 2

RESULT 340
PCT-US03-35845-61
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; Sequence 61, Application PC/TUS0335845
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11
; FILE REFERENCE: ISIS0008-500WO (HTS-0090WO)
; CURRENT APPLICATION NUMBER: PCT/US03/35845
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/293,863
; PRIOR FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
PCT-US03-35845-61

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1512 GAGAGCCAGAGCCAAA 1529
Db 2 GTGAGCCAGAGCCAAA 19

RESULT 341
US-08-465-866B-13/c
; Sequence 13, Application US/08465866B
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; TITLE OF INVENTION: Gapped Oligonucleotides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,866B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 244,993
; FILING DATE: 21-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-465-866B-13

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 342
US-08-756-806-27/c
; Sequence 27, Application US/08756806
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,806
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-756-806-27

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 343
US-09-996-263-13/c
; Sequence 13, Application US/09996263
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,263
FILING DATE: 28-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-996-263-13

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 344
US-10-057-550-28/c
; Sequence 28, Application US/10057550
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-28


```
Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 345
US-10-057-550A-27/c
; Sequence 27, Application US/10057550A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0625
; CURRENT APPLICATION NUMBER: US/10/057,550A
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550A-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 346
US-10-173-225B-27/c
; Sequence 27, Application US/10173225B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0655
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 27
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 347
US-10-266-090-45347/c
; Sequence 45347, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45347
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-45347

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGAGAGAGCAGC 1310
Db 20 GATGAGGAGAGAGCAGC 3

RESULT 348
US-10-293-863-27/c
; Sequence 27, Application US/10293863
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11
; FILE REFERENCE: HTS-0090
; CURRENT APPLICATION NUMBER: US/10/293,863
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-863-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
```


; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 16869
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2032440)...(2032457)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19728
US-10-367-892-16869

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTGCCT 1356
Db 17 TGACAAACGAATTGCCT 1

RESULT 359
PCT-US00-00654-44/c
; Sequence 44, Application PC/TUS00000654
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTSP-0044
; CURRENT APPLICATION NUMBER: PCT/US00/00654
; CURRENT FILING DATE: 2000-01-11
; EARLIER APPLICATION NUMBER: US 09/255,912
; EARLIER FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US00-00654-44

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1557 TGAATGGACCTCTCCAG 1573
Db 18 TGAATGGACCTCTACAG 2

RESULT 360
US-09-913-684-44/c
; Sequence 44, Application US/09913684
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTSP-0160
; CURRENT APPLICATION NUMBER: US/09/913,684
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 09/255,912
; PRIOR FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-913-684-44

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1557 TGAATGGACCTCTCCAG 1573
Db 18 TGAATGGACCTCTACAG 2

RESULT 361
US-10-349-143-5052/c
; Sequence 5052, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPL
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5052
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-20549 for SEQ 1118,
US-10-349-143-5052

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1469 AGAGGAGAGAGAAAGGAA 1485
Db 17 AGAGGAGAGAGAAATGGAA 1

RESULT 362
PCT-US03-05044-34
; Sequence 34, Application PC/TUS0305044
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short
; TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/108 (MEHB03-195)
; CURRENT APPLICATION NUMBER: PCT/US03/05044
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05

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; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 604
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-05044-34

Query Match          1.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 ACCAAGGAGGAGAGCC 1519
Db 2 ACCAUGGAGGAGAGCC 18

RESULT 363
PCT-US03-05044-311/c
; Sequence 311, Application PC/TUS0305044
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short
; TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/108 (MBHB03-195)
; CURRENT APPLICATION NUMBER: PCT/US03/05044
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 604
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05044-311

Query Match          1.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 ACCAAGGAGGAGAGCC 1519
Db 18 ACCATGGAGGAGAGCC 2

RESULT 364
US-10-310-188-16111
; Sequence 16111, Application US/10310188
```

```
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16111
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-16111

Query Match          0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1571 CAGCTCTGGCTTCCT 1585
Db 2 CAGCTCTGGCTTCCT 16

RESULT 365
US-10-266-090-38180
; Sequence 38180, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38180
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-38180

Query Match          0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GAGGACGAAGACGAC 1310
Db 4 GAGGACGAAGACGAC 18

RESULT 366
PCT-US00-06067-23
; Sequence 23, Application PC/TUS0006067
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16PC
; CURRENT APPLICATION NUMBER: PCT/US00/06067
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 09/264,908
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/265,992
; EARLIER FILING DATE: 1999-03-11
```



```
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Xu, Wen-feng
; APPLICANT: Grant, Francis J.
; APPLICANT: Foster, Donald C.
; APPLICANT: Kuijper, Joseph L.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16X
; CURRENT APPLICATION NUMBER: US/09/264,908
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-264-908-39
```

```
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
```

RESULT 371

```
US-09-265-117-22
; Sequence 22, Application US/09265117
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55X2
; CURRENT APPLICATION NUMBER: US/09/265,117
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-117-22
```

```
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
```

RESULT 372

```
US-09-265-117-39
; Sequence 39, Application US/09265117
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55X2
; CURRENT APPLICATION NUMBER: US/09/265,117
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-117-39
```

```
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
```

RESULT 373

```
US-09-265-992-23
; Sequence 23, Application US/09265992
; GENERAL INFORMATION:
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Xu, Wen-feng
; APPLICANT: Grant, Francis J.
; APPLICANT: Foster, Donald C.
; APPLICANT: Kuijper, Joseph L.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16X2
; CURRENT APPLICATION NUMBER: US/09/265,992
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-992-23
```

```
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
```

RESULT 374

```
US-09-347-930-22
; Sequence 22, Application US/09347930
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Raymond, Fenella C.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55X3
; CURRENT APPLICATION NUMBER: US/09/347,930
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-347-930-22
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGC 528
      |||||
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 375

```
US-09-347-930-39
; Sequence 39, Application US/09347930
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Raymond, Fenella C.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55X3
; CURRENT APPLICATION NUMBER: US/09/347,930
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-347-930-39
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGC 528
      |||||
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 376

```
US-09-628-127-22
; Sequence 22, Application US/09628127
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/09/628,127
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-628-127-22
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGC 528
      |||||
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 377

```
US-09-628-127-39
; Sequence 39, Application US/09628127
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/09/628,127
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-628-127-39
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGC 528
      |||||
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 378

```
US-10-243-072-22
; Sequence 22, Application US/10243072
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
```

```
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 379
US-10-243-072-39
; Sequence 39, Application US/10243072
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-39

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 380
US-10-310-188-23157/c
; Sequence 23157, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58290
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-58290

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGAAGAGGAGGAGGAGG 1396
Db 1 TGAAGAGGAGGAGAGATGG 18

RESULT 383
US-10-310-188-23178/c
; Sequence 23178, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23178
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23178
```

```
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23157
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23157

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 AGGAGAAAACCAAGGAGG 1512
Db 18 AGAAGAAAACCCAGGAGG 1

RESULT 381
US-10-310-188-23178/c
; Sequence 23178, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23178
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23178

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 AGGAGAAAACCAAGGAGG 1512
Db 18 AGAAGAAAACCCAGGAGG 1

RESULT 382
US-10-310-188-58290
; Sequence 58290, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58290
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-58290

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 AGGAGAAAACCAAGGAGG 1512
Db 18 AGAAGAAAACCCAGGAGG 1

RESULT 383
US-10-310-188-58290
; Sequence 58290, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58290
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-58290

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGAAGAGGAGGAGGAGG 1396
Db 1 TGAAGAGGAGGAGAGATGG 18

RESULT 383
US-10-310-188-23178/c
; Sequence 23178, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```

```
US-10-310-188-86028
; Sequence 86028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: US THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86028
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-86028
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 1 AGGAGGAGGAGACAGAG 18
|||||

RESULT 384
US-10-414-186-22
; Sequence 22, Application US/10414186
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
|||||

RESULT 385
US-10-414-186-39
; Sequence 39, Application US/10414186
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
|||||

RESULT 386
US-10-659-684-23
; Sequence 23, Application US/10659684
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZAPLHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-659-684-23
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
|||||
```



```
Db      1  ACTGGGCTGGGGGACTGC 18

RESULT 387
US-10-715-998-22
; Sequence 22, Application US/10715998
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/715,998
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-715-998-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511  ATTGGGCTGGGGCCTGC 528
Db      1  ACTGGGCTGGGGGACTGC 18

RESULT 388
US-10-715-998-39
; Sequence 39, Application US/10715998
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/715,998
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-715-998-39

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511  ATTGGGCTGGGGCCTGC 528
Db      1  ACTGGGCTGGGGGACTGC 18

RESULT 389
US-08-563-105-3/c
; Sequence 3, Application US/08563105
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Economides, Aris
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: HETEROMERIC RECEPTORS AND METHODS FOR
; TITLE OF INVENTION: THEIR PRODUCTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/563,105
; FILING DATE: 27-NOV-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,715
; FILING DATE: 14-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/140,222
; FILING DATE: 20-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-563-105-3

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      642  CACCATGGTGACGGCG 657
Db      16  CACCATGGTGCGGCG 1

RESULT 390
US-09-177-009-3/c
; Sequence 3, Application US/09177009
; GENERAL INFORMATION:
```

APPLICANT: Stahl, Neil
APPLICANT: Economides, Aris
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: HETEROMERIC RECEPTORS AND METHODS FOR
TITLE OF INVENTION: THEIR PRODUCTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,009
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/563,105
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: US 60/006,715
FILING DATE: 14-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,222
FILING DATE: 20-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-09-177-009-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
| | | | | | | | | | | | | | | |
Db 16 CACCATGGTGCGGGCG 1

RESULT 391
US-09-708-690-5827
; Sequence 5827, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08

PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 09/685,664
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 20828
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5827
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-09-708-690-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCGCTGCACCA 532
| : | | | | | | | | | | | | | | | |
Db 1 CUGGGAGCCUGCACCA 16

RESULT 392
US-09-787-835-3/c
; Sequence 3, Application US/09787835
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/09/787,835
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-09-787-835-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
| | | | | | | | | | | | | | | |
Db 16 CACCATGGTGCGGGCG 1

RESULT 393
US-09-870-161-5827
; Sequence 5827, Application US/09870161
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-M (400/026)
; CURRENT APPLICATION NUMBER: US/09/870,161
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 20821
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827

```

; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-870-161-5827

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      517 CTGGGGCCTGCACCA 532
      |:|:|:|:|:|:|:|:|
Db      1 CUGGGAGCCUGCACCA 16

RESULT 394
US-09-935-868-3/c
; Sequence 3, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-09-935-868-3

```

```

Query Match          0.9%;   Score 14.4;   DB 1;   Length 16;
Best Local Similarity 93.8%;   Pred. NO. 2.6e+02;
Matches 15;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      642  CACCATGGTGACGGCG 657
          |||||
Db      16  CACCATGGTGCGGCG 1

```

```

RESULT 395
US-10-138-674-5827
; Sequence 5827, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5827

```

Query Match	0.9%	Score 14.4;	DB 1;	Length 16;
Best Local Similarity	81.2%;	Pred. NO. 2.6e+02;		
Matches 13;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
QY	517	CTGGGGGCGCTGCACCA	532	
		: : : : : : : :		
Db	1	CUGGGAGCCUGCACCA	16	

```

; LIFE: NAME
; ORGANISM: Homo sapiens
US-09-870-161-5827

Query Match          0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      517 CTGGGGGCGCTGCACCA 532
      ||:|||||:|||||
Db       1 CUGGGAGCCGCGACCA 16

RESULT 394
US-09-935-868-3/c
; Sequence 3, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11

```

```

; PRIOR APPLICATION NUMBER: PCI/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

US-09-935-868-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best local Similarity 93.8%; Pred. NO. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OTHER INFORMATION: NOZAK sequence

QY 642 CACCATGGTGACGGCG 657
 |||||
 Db 16 CACCATGGTGCGCG 1

RESULT 395
 US-10-138-674-5827
 ; Sequence 5827, Application US/10138674
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHR00-876-N (400/049)

```

;
; CURRENT FILING DATE: 2002-05-03
; CURRENT APPLICATION NUMBER: US/10/138,674
;
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
;

```

Query Match	0.9%	Score 14.4;	DB 1;	Length 16;
Best Local Similarity	81.2%	Pred. NO. 2.6e+02;		
Matches 13;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
QY	517	CTGGGGGCCCTGCACCA	532	
db	1	CTGGGAGCCTTGCACCA	16	

FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Kozak sequence
US-10-287-035-3
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGCGGCG 1
RESULT 399
US-10-287-949A-5827
Sequence 5827, Application US/10287949A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5827
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-5827
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CUGGAGCCUGCACCA 16
RESULT 400
US-10-310-188-39096
Sequence 39096, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39096
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-39096
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1383 GAGGAGGGGAGGGGG 1398
Db 1 GAGGAGGGGAGGGGG 16
RESULT 401
PCT-US01-29656-779/c
Sequence 779, Application PC/TUS0129656
GENERAL INFORMATION:
APPLICANT: ZHANG, Jian
APPLICANT: AEOMICA, INC.
TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1
FILE REFERENCE: AEOMICA-18 PCT
CURRENT APPLICATION NUMBER: PCT/US01/29656
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/315,676
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: GB 0024263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 2034
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 779
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-29656-779

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1247 CCAAACGCACGCGATT 1262
Db 17 CCAAATGCACGCGATT 2

```

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 678
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
PCT-US02-17674-678

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      516 GCTGGGGGCGCTGCACC 531
      ||:|||||:|||||
DB       2 GCUGGGAGCCUGCACC 17

RESULT 404
PCT-US02-25940-19155/c
; Sequence 19155, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2327709)...(2327725)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber
PCT-US02-25940-19155

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY      1340 TGACAAACGAATTGCC 1355
      |||||||:|||||
DB       16 TGACAAAGAAATTGCC 1

RESULT 405
US-09-541-946-1695
; Sequence 1695, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE

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; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3282
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-3282

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1418 CTTCAAAAAAGCCAAG 1433
Db      17 CTTCAATAAGCCAAG 2

RESULT 408
US-09-546-745A-3285/c
; Sequence 3285, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3285
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-3285

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1415 CCACTTCAAAAAAGCC 1430
Db      16 CCACTTCAATAAGCC 1

RESULT 409
US-09-708-690-4754
; Sequence 4754, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Condit
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772

```

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; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-4754

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      517 CTGGGGGCGCTGCACCA 532
Db      1  CUGGGAGCCUGCACCA 16

RESULT 410
US-09-708-690-7632
; Sequence 7632, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-7632

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      516 GCTGGGGGCGCTGCACC 531
Db      2  GCUGGGAGCCUGCACCC 17

RESULT 411
US-09-780-164-387/c
; Sequence 387, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 387
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-387

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1119 TTGGACCAGATTTC A 1134
Db      17 TTGGACCAGATTGCA 2

RESULT 412
US-09-780-164-966/c
; Sequence 966, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 966
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-966

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1119 TTGGACCAGATTTC A 1134
Db      16 TTGGACCAGATTGCA 1

RESULT 413
US-09-870-161-4754
; Sequence 4754, Application US/09870161
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-M (400/026)
; CURRENT APPLICATION NUMBER: US/09/870,161
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 20821
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-870-161-4754

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      517 CTGGGGGCGCTGCACCA 532
```



```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674A-7632

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGCCTGCACC 531
Db 2 GCUGGAGCCUGCACC 17

RESULT 419
US-10-227-563-19155/c
; Sequence 19155, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2327709) ... (2327725)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22452
US-10-227-563-19155
```

```
Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTGCC 1355
Db 16 TGACAAAGAAATTGCC 1
```

```
RESULT 420
US-10-287-949A-4754
; Sequence 4754, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4754
```

```
Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 517 CTGGGGGCCTGCACCA 532
Db 1 CUGGAGCCUGCACCA 16
```

```
RESULT 421
US-10-287-949A-7632
; Sequence 7632, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7632
```

```
Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 516 GCTGGGGCCTGCACC 531
Db 2 GCUGGAGCCUGCACC 17
```

```
RESULT 422
US-10-310-188-18308
; Sequence 18308, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18308
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18308
```

```
Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1383 GAGGAGGGAGAGGGGG 1398
Db 2 GAGGAGGGAGAGGGAG 17
```

```
RESULT 423
US-10-367-892-19155/c
; Sequence 19155, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
```

FEATURE:
LOCATION: (2327709)....(2327725)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22452
US-10-367-892-19155

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTGCC 1355
|||
Db 16 TGACAAAGCAATTGCC 1

RESULT 424
US-10-712-633-678
Sequence 678, Application US/10712633
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pamela
APPLICANT: Sandberg, Jennifer
APPLICANT: Gordon, Gilad
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
FILE REFERENCE: MBHB02-325PCT (400/047)
CURRENT APPLICATION NUMBER: US/10/712,633
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 09/708,690
PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: US 09/870,161
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/334,461
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/138,674
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: PatentIn version 3.0
SEQ ID NO 678
LENGTH: 17
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-712-633-678

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGCGCTGCACC 531
|||
Db 2 GCUGGAGCCUGCACC 17

RESULT 425
US-10-723-361-971/c
Sequence 971, Application US/10723361
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105

CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 971
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-361-971

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCCTG 527
|||||
Db 17 TTGGGCTGGGGCCTG 2

RESULT 426
US-10-723-361-972/c
Sequence 972, Application US/10723361
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART P
FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30


```

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-7223-361-972

```

Query Match	0.9%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity	93.8%;	Pred. No. 2.8e+02;		
Matches 15;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
Qy	512	TTGGGCTGGGGCCTG	527	
db	16	TTGGGCTTGGGGCCTG	1	

RESULT 427
US-60-315-676-779/c
; Sequence 779, Application US/60315676
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1

```

; FILE REFERENCE: AEOMICA-18
; CURRENT APPLICATION NUMBER: US/60/315,676
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: GB 0024263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 2034
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 779
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-60-315-676-779

```

Query Match	0.9%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity	93.8%;	Pred. No. 2.8e+02;		
Matches 15;	Conservative	0;	Mismatches 1;	Indels 0;
				Caps 0;

Qy 1247 CCAAACGCAGCGATT 1262
Db 17 CCAATGCAGCGATT 2

RESULT 428
US-60-315-676-780/c
; Sequence 780, Application US/60315676
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1
; FILE REFERENCE: AEOmica-18
; CURRENT APPLICATION NUMBER: US/60/315,676
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: GB 0024263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 2034
; SOFTWARE: Aeo mica Sequence Listing Engine
; SEQ ID NO 780
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-315-676-780

Query Match	0.9%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity	93.8%;	Pred. No. 2.8e+02;		
Matches 15; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1247 CCAAACGCAGCGATT 1262
||| ||| ||| ||| |||
Db 16 CCAATGCAGCGATT 1

```

RESULT 429
US-60-339-764-2348/c
; Sequence 2348, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEOMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2348
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2348

```

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
Db 17 AAACCAAGGAGGAGCA 2

RESULT 430

US-60-339-764-2349/c
Sequence 2349, Application US/60339764

GENERAL INFORMATION:

APPLICANT: Guo, Jinjiao
TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1

FILE REFERENCE: AEOMICA-31

CURRENT APPLICATION NUMBER: US/60/339,764

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 3310

SOFTWARE: Aecomica Sequence Listing Engine

SEQ ID NO 2349

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-60-339-764-2349

Query Match

Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
Db 16 AAACCAAGGAGGAGCA 1

RESULT 431

US-08-406-779-74/c

Sequence 74, Application US/08406779

GENERAL INFORMATION:

APPLICANT: AHRWEILER, PATRICIA

APPLICANT: MOORE, MARGARET

TITLE OF INVENTION: ALTERED AFFINITY POLYPEPTIDES OF METAL

TITLE OF INVENTION: CHELATE BINDING ANTIBODIES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL AND FLORES

STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: UNITED STATES

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,779

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/975,230

FILING DATE: 12-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.

REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: P-HY 9411

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
US-08-406-779-74

Query Match

Best Local Similarity 0.9%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 611 CCAGAGGGTGCTGTAC 626
Db 18 CCAGAGGTGCTGTAC 3

RESULT 432

US-08-803-305-4/c

Sequence 4, Application US/08803305

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmsberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/803,305

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other

IMMEDIATE SOURCE:

CLONE: ZC11107

US-08-803-305-4

Query Match

Best Local Similarity 0.9%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470

Db 17 AAAGAGAAACCCAG 2

RESULT 433

US-08-803-305A-4/c

Sequence 4, Application US/08803305A

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmsberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/803,305A

FILING DATE: 20-FEB-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other

IMMEDIATE SOURCE:

CLONE: ZC11107

US-08-803-305A-4

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAACCCAG 1470

Db 17 AAAGAGAAACCCAG 2

RESULT 434

US-09-275-712-4/c

Sequence 4, Application US/09275712

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmsberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: Class II Cytokine Receptor-7

FILE REFERENCE: 96-24D1

CURRENT APPLICATION NUMBER: US/09/275,712

EARLIER FILING DATE: 1999-03-24

EARLIER APPLICATION NUMBER: 08/943,087

EARLIER FILING DATE: 1997-10-02

EARLIER APPLICATION NUMBER: 08/803,305

EARLIER FILING DATE: 1997-02-20

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 18

TYPE: DNA

ORGANISM: Homo sapiens

US-09-275-712-4

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAACCCAG 1470

Db 17 AAAGAGAAACCCAG 2

RESULT 435

US-09-463-075A-165

Sequence 165, Application US/09463075A

GENERAL INFORMATION:

APPLICANT: COHEN, Daniel

BLUMENFELD, Marta

TCHOUMAKOV, Ilia

TITLE OF INVENTION: Biallelic markers for use in constructing a high density disequilibrium map of the human genome.

NUMBER OF SEQUENCES: 336

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 550 West C Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Win95

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/463,075A

FILING DATE: 14-Jan-2000

INFORMATION FOR SEQ ID NO: 165:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65

LOCATION: 1..18

SEQUENCE DESCRIPTION: SEQ ID NO: 165:

US-09-463-075A-165

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAG 1472

Db 1 AGAGAAAGACCCAG 16

```
RESULT 436
US-10-269-557-46
; Sequence 46, Application US/10269557
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/10/269,557
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/207,388
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Used to clone Neisseria meningitidis Hsp70
; OTHER INFORMATION: gene and to construct Neisseria meningitidis Hsp70
; OTHER INFORMATION: expression vectors
US-10-269-557-46

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AAGCCAATGCTGAGGA 298
Db 2 AAGCCAATGCCGAGGA 17

RESULT 437
US-10-303-778-7630/c
; Sequence 7630, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7630
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-7630

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1380 GAAGAGGAGGGAGAGG 1395
Db 18 GAAGAGGAGTGAGAGG 3

RESULT 438
US-10-303-778-8260
; Sequence 8260, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8260
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-8260

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGGC 1400
Db 3 GGAGGGAGAGGGGGGC 18

RESULT 439
US-10-310-188-14763
; Sequence 14763, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14763
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-14763

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGGC 1400
Db 3 GGAGGGAGAGGGGGGC 18

RESULT 440
US-10-310-188-18291
; Sequence 18291, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18291
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18291

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1383 GAGGAGGGAGAGGGGG 1398
Db 3 GAGGAGGGAGAGGGAG 18

RESULT 441
US-10-310-188-29093/c
; Sequence 29093, Application US/10310188
```

GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29093
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-29093

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 587 CATCCTGGAAGTCTA 602
|||||
Db 16 CATCCAGGAAGTCTA 1

RESULT 442
US-10-310-188-35240
Sequence 35240, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35240
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-35240

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GAGGAGAAGAAAGGAA 1485
|||||
Db 1 GAGGAGAAGAAAGGAA 16

RESULT 443
US-10-310-188-86025
Sequence 86025, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 86025
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-86025

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GAGGAGAAGAAAGGAA 1485
|||||
Db 2 GAGGAGAAGCAAGGAA 17

RESULT 444
US-10-310-188-86059
Sequence 86059, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 86059
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-86059

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1506 AAGGAGGAGAGCCAG 1521
|||||
Db 3 AAGGAGGAGAGCCAG 18

RESULT 445
US-10-349-143-4102
Sequence 4102, Application US/10349143
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4102
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-13273 for SEQ 168,
US-10-349-143-4102

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTCTGGGTCTCTG 16
|||||
Db 1 ATGTCTGGGTCTCTG 16

RESULT 446
US-10-349-143-9179

; Sequence 9179, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9179
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-2275 for SEQ 1314, in compleme
US-10-349-143-9179

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAG 1472
|||||
Db 1 AGAGAAAGAACCCAGAG 16

RESULT 447
US-10-367-438-165
; Sequence 165, Application US/10367438
; GENERAL INFORMATION:
; APPLICANT: COHEN, Daniel
; BLUMENFELD, Marta
; TCHOUMAKOV, Iliia
; TITLE OF INVENTION: Biallelic markers for use in
; constructing a high density disequilibrium map of
; the human genome.

NUMBER OF SEQUENCES: 336
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/367,438
FILING DATE: 14-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/463,075A
FILING DATE: 14-Jan-2000

INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-10-367-438-165

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAG 1472
|||||
Db 1 AGAGAAAGAACCCAGAG 16

RESULT 448
US-10-636-716-4/c
; Sequence 4, Application US/10636716
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:
CLONE: ZC11107

US-10-636-716-4
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
|||||
Db 17 AAAGAGAAACACCCAG 2

RESULT 449

US-60-082-614-2026
; Sequence 2026, Application US/60082614

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfeld, Marta
TITLE OF INVENTION: Biallelic markers for use in constructing a
TITLE OF INVENTION: high density disequil
NUMBER OF SEQUENCES: 2730
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92101-3505

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/60/082,614
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: GENSET.020PR
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 2026:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: downstream amplification primer for SEQ ID67 and SEQ ID720
LOCATION: 1..18

US-60-082-614-2026

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAG 1472

|||||

Db 1 AGAGAAAGACCCAG 16

Search completed: June 24, 2004, 10:20:06
Job time : 10 secs

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:08:20 ; Search time 4 Seconds
(without alignments)
3.688 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgcccgcg.....tcctcacgtttctttccc 1611

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5
Searched: 244 seqs, 4578 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 244 summaries

Database : . rng2.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	27	1.7	27	1	ABZ83012
2	26	1.6	26	1	AAA55804
3	26	1.6	26	1	AAH43114
4	26	1.6	26	1	AAC89534
5	26	1.6	26	1	AAC89543
6	25.4	1.6	27	1	ABZ83014
7	24.4	1.5	26	1	AAC89541
8	24.4	1.5	26	1	AAC89533
9	24.4	1.5	26	1	AAC89532
10	24.4	1.5	26	1	AAC89542
11	23.4	1.5	26	1	AAA55837
12	23.4	1.5	26	1	AAA55838
13	23	1.4	23	1	AAA55802
14	23	1.4	23	1	AAH43112
15	22.8	1.4	26	1	AAA55810
16	22.8	1.4	26	1	AAH43120
17	22.8	1.4	26	1	AAC89535
18	22.8	1.4	26	1	AAC89544
19	22	1.4	22	1	AAA55803
20	22	1.4	22	1	AAH43113
21	21.4	1.3	23	1	AAA55808
22	21.4	1.3	23	1	AAH43118
23	20.4	1.3	22	1	AAA55809
24	20.4	1.3	22	1	AAH43119
25	20	1.2	20	1	AAA55793
26	20	1.2	20	1	AAA55792
27	20	1.2	20	1	AAA55794
28	20	1.2	20	1	AAA55800
29	20	1.2	20	1	AAA55795
30	20	1.2	20	1	AAA55796
31	20	1.2	20	1	AAA55801
32	20	1.2	20	1	AAA55798
33	20	1.2	20	1	AAH43108
34	20	1.2	20	1	Antisense oligo, t
35	20	1.2	20	1	Antisense oligo, t
36	20	1.2	20	1	Antisense oligo, t
37	20	1.2	20	1	Antisense oligo, t
38	20	1.2	20	1	Antisense oligo, t
39	20	1.2	20	1	Antisense oligo, t
40	20	1.2	20	1	Antisense oligo, t
41	20	1.2	20	1	Human HDAC-1 antis
42	20	1.2	20	1	Human HDAC-1 PCR p
43	20	1.2	20	1	Human histone deac
44	20	1.2	20	1	Human histone deac
45	20	1.2	20	1	Human HDAC1 antis
46	20	1.2	20	1	Human HDAC1 antis
47	20	1.2	20	1	Human HDAC1 antis
48	20	1.2	20	1	Human HDAC1 antis
49	20	1.2	20	1	Human HDAC1 antis
50	20	1.2	20	1	Human HDAC1 antis
51	20	1.2	20	1	Human HDAC1 antis
52	20	1.2	20	1	Human HDAC1 antis
53	20	1.2	20	1	Human HDAC1 antis
54	20	1.2	20	1	Human HDAC1 antis
55	20	1.2	20	1	Human HDAC1 antis
56	20	1.2	20	1	Human HDAC1 antis
57	20	1.2	20	1	Human HDAC1 antis
58	20	1.2	20	1	Human HDAC1 antis
59	20	1.2	20	1	Human HDAC1 antis
60	20	1.2	20	1	Human HDAC1 antis
61	20	1.2	20	1	Human HDAC1 antis
62	20	1.2	20	1	Human HDAC1 antis
63	20	1.2	20	1	Human HDAC1 antis
64	20	1.2	20	1	Human HDAC1 antis
65	20	1.2	20	1	Human HDAC1 antis
66	20	1.2	20	1	Human HDAC1 antis
67	20	1.2	20	1	Human HDAC1 antis
68	20	1.2	20	1	Human HDAC1 antis
69	20	1.2	20	1	Human HDAC1 antis
70	20	1.2	20	1	Human HDAC1 antis
71	20	1.2	20	1	Human HDAC1 antis
72	20	1.2	20	1	Human HDAC1 antis
73	20	1.2	20	1	Human HDAC1 antis
74	20	1.2	20	1	Human HDAC1 antis
75	20	1.2	20	1	Human HDAC1 antis
76	20	1.2	20	1	Human HDAC1 antis
77	20	1.2	20	1	Human HDAC1 antis
78	20	1.2	20	1	Human HDAC1 antis
79	20	1.2	20	1	Human HDAC1 antis
80	20	1.2	20	1	Human HDAC1 antis
81	20	1.2	20	1	Human HDAC1 antis
82	20	1.2	20	1	Human HDAC1 antis
83	20	1.2	20	1	Human HDAC1 antis
84	20	1.2	20	1	Human HDAC1 antis
85	20	1.2	20	1	Human HDAC1 antis
86	20	1.2	20	1	Human HDAC1 antis
87	20	1.2	20	1	Human HDAC1 antis
88	20	1.2	20	1	Human HDAC1 antis
89	20	1.2	20	1	Human HDAC1 antis
90	20	1.2	20	1	Human HDAC1 antis
91	20	1.2	20	1	Human HDAC1 antis
92	20	1.2	20	1	Human HDAC1 antis
93	20	1.2	20	1	Human HDAC1 antis
94	20	1.2	20	1	Human HDAC1 antis
95	20	1.2	20	1	Human HDAC1 antis
96	20	1.2	20	1	Human HDAC1 antis
97	20	1.2	20	1	Human HDAC1 antis
98	20	1.2	20	1	Human HDAC1 antis
99	20	1.2	20	1	Human HDAC1 antis
100	20	1.2	20	1	Human HDAC1 antis
101	20	1.2	20	1	Human HDAC1 antis
102	20	1.2	20	1	Human HDAC1 antis
103	20	1.2	20	1	Human HDAC1 antis
104	19.2	1.2	24	1	Human HDAC-1 antis
105	18.4	1.1	20	1	Human histone deac
106	18.4	1.1	20	1	Human histone deac

C 107	18.4	1.1	20	1	AAH43107	Antisense oligo, t	180	13.8	0.9	17	1	ABV79344	Human HTPL scannin
C 108	18.4	1.1	20	1	AAH43109	Antisense oligo, t	181	13.8	0.9	17	1	ABV79345	Human HTPL scannin
C 109	18.4	1.1	20	1	AAD40902	Human HDA1 antisen	182	13.8	0.9	17	1	ABV79343	Human HTPL scannin
C 110	18.4	1.1	20	1	AAD40927	Human HDA1 antisen	183	13.8	0.9	17	1	ABK18013	Human ERG hammerhe
C 111	17	1.1	17	1	ABT39526	Tumour suppression	184	13.8	0.9	17	1	ABK18165	Human ERG hammerhe
C 112	17	1.1	17	1	ABT39292	Tumour suppression	185	13.8	0.9	17	1	ABN85838	Related to Bombyx
C 113	17	1.1	21	1	AAV67421	Nucleotide fragmen	C 186	13.8	0.9	17	1	ABL31482	Human HLA genotypi
C 114	16.8	1.0	20	1	ABQ93091	T. tauschii/wheat	C 187	13.8	0.9	17	1	ABK55737	Human CLCA1 gene e
C 115	16.8	1.0	20	1	ABZ92578	Human oligonucleot	C 188	13.8	0.9	17	1	ABT21381	Multiplex group PC
C 116	16.8	1.0	20	1	ACC86770	Human VEGFR-1 chim	189	13.8	0.9	17	1	ABZ65102	Human HER2 DNzyme
C 117	16.8	1.0	20	1	ACC44266	5' primer to ampli	190	13.8	0.9	17	1	ABZ61604	Human H-Ras DNzyme
C 118	16.6	1.0	17	1	ADD94313	Mouse HUI77/HUIV26	191	13.8	0.9	17	1	ABZ61695	Human H-Ras DNzyme
C 119	16.4	1.0	20	1	AAT27507	Human c-raf kinase	192	13.8	0.9	17	1	ACD62482	HCV minus strand D
C 120	16.4	1.0	20	1	AAZ36464	Chimeric 2'-O-meth	C 193	13.8	0.9	17	1	ACD60187	HCV DNzyme substr
C 121	16.4	1.0	20	1	AAT59728	Human raf inhibito	194	13.8	0.9	17	1	ACD65057	HCV minus strand D
C 122	16.4	1.0	20	1	AAT62157	Human c-raf and de	C 195	13.8	0.9	17	1	ACD62411	HCV minus strand D
C 123	16.4	1.0	20	1	AAZ15070	c-raf antisense ch	C 196	13.8	0.9	17	1	ACD51143	HBV hammerhead rib
C 124	16.4	1.0	20	1	AAZ11537	Human c-raf kinase	197	13.8	0.9	17	1	ACD60202	HCV DNzyme substr
C 125	16.4	1.0	20	1	AAZ05468	Chimeric antisense	C 198	13.8	0.9	17	1	ACC63240	Murine oligonucleo
C 126	16.4	1.0	20	1	AAZ10296	Oligonucleotide us	C 199	13.8	0.9	17	1	ACC68438	Murine oligonucleo
C 127	16.4	1.0	20	1	AAZ48166	C-raf chimeric pho	C 200	13.8	0.9	17	1	ADB42595	Tumour suppression
C 128	16.4	1.0	20	1	AAZ73515	c-raf kinase antis	C 201	13.8	0.9	17	1	ADB42646	Tumour suppression
C 129	16.4	1.0	20	1	AAD44740	Human c-raf kinase	C 202	13.8	0.9	17	1	ADC04842	Human Na/H exchang
C 130	16.4	1.0	20	1	ACD42099	Antisense oligonuc	C 203	13.8	0.9	17	1	ADD80993	Rabbit beta-globin
C 131	16.4	1.0	20	1	ACA61359	Human c-raf mRNA a	C 204	13.4	0.8	15	1	AAF48241	IGFBP3 oligonucleo
C 132	16.4	1.0	20	1	ADD44696	Human c-Raf antis	C 205	13.4	0.8	15	1	AAF45342	IGFBP2 oligonucleo
C 133	15.4	1.0	17	1	AAF03299	Hammerhead ribozym	C 206	13.4	0.8	15	1	AAF49639	IGF-I oligonucleot
C 134	15.4	1.0	17	1	AAF03298	Hammerhead ribozym	C 207	13.4	0.8	15	1	AAF49640	IGF-I oligonucleot
C 135	15.4	1.0	18	1	AAZ10583	Smad2 antisense ol	C 208	13.4	0.8	15	1	AAF49372	IGF-I oligonucleot
C 136	15.4	1.0	18	1	AAZ70698	Human biallelic ma	C 209	13.4	0.8	15	1	AAF52624	IGF-I oligonucleot
C 137	15	0.9	15	1	AAF53136	IGF-I oligonucleot	210	13.4	0.8	15	1	AAF53134	IGF-I oligonucleot
C 138	14.8	0.9	18	1	AAZ22495	Streptomyces sp. e	211	13.4	0.8	15	1	AAF49638	IGF-I oligonucleot
C 139	14.8	0.9	18	1	AAV00348	Insecticidal gene	212	13.4	0.8	15	1	ABK81387	SCYA21 gene allele
C 140	14.8	0.9	18	1	AAZ94539	Human cytokine rec	C 213	13.4	0.8	16	1	AAQ96309	p53 gene hybridisa
C 141	14.8	0.9	18	1	AAZ73266	Oligonucleotide #5	C 214	13	0.8	13	1	ABF45449	Oligonucleotide SE
C 142	14.8	0.9	18	1	AAZ20658	Human zalphall1 rec	C 215	13	0.8	13	1	ABF51968	Oligonucleotide SE
C 143	14.8	0.9	18	1	AAD61901	Human zalphall1 DNA	C 216	13	0.8	13	1	ABF45448	Oligonucleotide SE
C 144	14.8	0.9	18	1	AAD61918	Human MPL-Zalphall	C 217	13	0.8	13	1	ABF51969	Oligonucleotide SE
C 145	14.4	0.9	17	1	AAZ72366	Single nucleotide	C 218	13	0.8	14	1	AAT14275	IL-4 and/or IL-13
C 146	14.4	0.9	17	1	AAZ72375	Single nucleotide	C 219	13	0.8	14	1	AAT14274	IL-4 and/or IL-13
C 147	14.4	0.9	17	1	AAF03297	Hammerhead ribozym	C 220	13	0.8	14	1	AAT41588	Cytokine activated
C 148	14.4	0.9	17	1	AAF03300	Hammerhead ribozym	C 221	13	0.8	14	1	AAV61625	Regulatory element
C 149	14.4	0.9	17	1	ABK03667	Human CD20 Amberzy	C 222	13	0.8	14	1	AAV61626	Regulatory element
C 150	14.4	0.9	17	1	ABK03088	Human CD20 Inozyme	C 223	13	0.8	15	1	AAQ51221	Vaccinia regulator
C 151	14.4	0.9	17	1	ABN00979	Human GDMPLP-1 17-m	C 224	13	0.8	15	1	AAQ51221	Human rela hammerh
C 152	14.4	0.9	17	1	ABN00980	Human GDMPLP-1 17-m	C 225	13	0.8	15	1	AAQ51221	Human CETP HH ribo
C 153	14.4	0.9	17	1	ABQ64004	Human KTM1a porti	C 226	13	0.8	15	1	AAQ51221	Human CETP HH ribo
C 154	14.4	0.9	17	1	ABQ64003	Human KTM1a porti	C 227	13	0.8	15	1	AAV28329	DNA EDTA probe (7)
C 155	14.4	0.9	18	1	AAQ11746	Target duplex from	C 228	13	0.8	15	1	AAV48734	ErbB-2 gene antise
C 156	14.4	0.9	18	1	AAQ68779	CHA255 light chain	C 229	13	0.8	15	1	AAQ51318	Tag sequence of a
C 157	14.4	0.9	18	1	AAV57517	Zcytor7 cytokine r	C 230	13	0.8	15	1	AAQ51318	IGF-I oligonucleot
C 158	14.4	0.9	18	1	AAZ52697	Human genome biall	C 231	13	0.8	15	1	AAQ51318	IGFBP3 oligonucleo
C 159	14.4	0.9	18	1	AAA49365	Sequencing primer	C 232	13	0.8	15	1	AAQ51318	IGFBP3 oligonucleo
C 160	14.4	0.9	18	1	AAZ69746	Human biallelic ma	C 233	13	0.8	15	1	AAQ51318	Solute Carrier Fam
C 161	14.4	0.9	18	1	AAZ74823	Human biallelic ma	C 234	13	0.8	15	1	ABK55779	Human CFL1 ASO PCR
C 162	14	0.9	15	1	AAF53137	IGF-I oligonucleot	C 235	13	0.8	15	1	ABQ86675	Human N-acetylgala
C 163	14	0.9	15	1	ACC67627	IGF-I oligonucleot	C 236	13	0.8	15	1	ABT05320	DNA-templated synt
C 164	14	0.9	17	1	ACC67627	Murine oligonucleo	C 237	13	0.8	15	1	ABK56592	Human interleukin
C 165	13.8	0.9	17	1	AAZ69652	Human flt1 VEGF re	C 238	13	0.8	15	1	ABZ34008	HIV-1 reverse tran
C 166	13.8	0.9	17	1	AAZ73006	Mouse flk-1 VEGF r	C 239	13	0.8	15	1	ABK32272	Human colon cancer
C 167	13.8	0.9	17	1	AAZ62242	Granule bound star	C 240	13	0.8	15	1	ABK32272	Human PCDH2 ASO PC
C 168	13.8	0.9	17	1	AAA17513	Aryl hydrocarbon n	C 241	13	0.8	16	1	AAQ40937	Sense running star
C 169	13.8	0.9	17	1	AAZ93921	Primer (EP1/11RT)	C 242	13	0.8	16	1	AAQ40937	PUR element conser
C 170	13.8	0.9	17	1	AAZ61360	Human FP and EP1 r	C 243	13	0.8	16	1	ABZ72358	Gene 216 polymorph
C 171	13.8	0.9	17	1	AAF02125	Hammerhead ribozym	C 244	13	0.8	16	1	ABX75211	Human 216 gene all
C 172	13.8	0.9	17	1	ABL46462	Human GRID hammerh							
C 173	13.8	0.9	17	1	AAH80102	Oligonucleotide hy							
C 174	13.8	0.9	17	1	ABN06570	Human GDMPLP-1 17-m							
C 175	13.8	0.9	17	1	ABN07092	Human GDMPLP-1 17-m							
C 176	13.8	0.9	17	1	ABN08676	Human GDMPLP-1 17-m							
C 177	13.8	0.9	17	1	ABN08675	Human GDMPLP-1 17-m							
C 178	13.8	0.9	17	1	ABQ63445	Human KTM1a porti							
C 179	13.8	0.9	17	1	ABV79342	Human HTPL scannin							

ALIGNMENTS

RESULT 1
ABZ83012
ID ABZ83012 standard; DNA; 27 BP.

XX ABZ83012;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human PCR primer #171.
XX
DE Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
KW Homo sapiens.
XX
OS Synthetic.
OS
PN WO2003016500-A2.
XX
XX 27-FEB-2003.
PD
XX
PF 16-AUG-2002; 2002WO-US026514.
XX
XX 16-AUG-2001; 2001US-0313080P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
PI Alen P;
PI
XX WPI; 2003-269322/26.
DR
XX Determining a toxicological response to an agent, useful for screening of
XX drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
PT
XX Claim 1; Page 99; 455pp; English.
PS
XX The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in ABZ82842
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ Sequence 27 BP; 7 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 1.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1047 ACATATGAGACAGCTGTGGCCCTGGAT 1073
DB 1 ACATATGAGACAGCTGTGGCCCTGGAT 27
RESULT 2
AAA55804/c
ID AAA55804 standard; DNA; 26 BP.
XX
AC AAA55804;

XX 01-SEP-2000 (first entry)
DT
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:47.
XX
KW Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
OS
PN WO2000023112-A1.
XX
XX 27-APR-2000.
PD
XX 19-OCT-1999; 99WO-US024278.
PF
XX 19-OCT-1998; 98US-0104804P.
PR
XX (METH-) METHYLGENE INC.
PA
XX Besterman JM, Macleod AR, Siders WM;
PI
XX WPI; 2000-339532/29.
DR
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
PT
XX Example 9; Page 29; 99pp; English.
PS
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
DB 26 GAATCCGCATGACTCATAATTGCTG 1
RESULT 3
AAH43114/c
ID AAH43114 standard; DNA; 26 BP.
XX
XX

AC AAH433114;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 211-236.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 4
AAC89534/c
ID AAC89534 standard; DNA; 26 BP.
XX
AC AAC89534;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 4.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.

XX 03-MAY-1999; 99US-0132287P.
PR (METH-) METHYLGENE INC.
XX
PA Macleod AR, Li Z, Besterman JM;
XX
PI WPI; 2001-016407/02.
XX
DR Antisense oligonucleotide that inhibits expression of a histone
XX deacetylase, useful for treating and/or alleviating the symptoms of
XX neoplasia, or for inhibiting neoplastic cell growth in an animal.
PT
PT Example 2; Page 12; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 5
AAC89543/c
ID AAC89543 standard; DNA; 26 BP.
XX
AC AAC89543;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 13.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX
PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX Example 1; Page 23; 125pp; English.
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 11;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATAAATTTGCTG 236
 |||||
 Db 26 GAATCCGATGACTCATAAATTTGCTG 1

RESULT 11
 AAA55837/c
 ID AAA55837 standard; DNA; 26 BP.
 XX
 AC AAA55837;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:82.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Besterman JM, Macleod AR, Siders WM;
 XX
 DR WPI; 2000-339532/29.
 XX
 PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Example 9; Page 58; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention
 XX
 SQ Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 1.5%; Score 23.4; DB 1; Length 26;
 Best Local Similarity 96.0%; Pred. No. 15;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATAAATTTGCTG 236
 |||||
 Db 25 AATCCGATGACCCATAAATTTGCTG 1

RESULT 12
 AAA55838/c
 ID AAA55838 standard; DNA; 26 BP.
 XX
 AC AAA55838;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:83.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Besterman JM, Macleod AR, Siders WM;
 XX
 DR WPI; 2000-339532/29.
 XX
 PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Example 9; Page 58; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention
 XX

SQ Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;
Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 15;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 212 AATCCGCATGACTCATAAATTCGCTG 236
Db 25 AATCCGCATGACTCATAAATTCGCTG 1
RESULT 13
AAAS5802/c
ID AAAS5802 standard; DNA; 23 BP.
XX
AC AAAS5802;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:45.
XX
KW Human; DNA methyltransferase; DNA MeTase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;
XX
DR WPI; 2000-339532/29.
XX
PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
XX
CC The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAAS5758 to AAAS5842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention

XX
SQ Sequence 23 BP; 6 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1
RESULT 14
AAH43112/c
ID AAH43112 standard; DNA; 23 BP.
XX
AC AAH43112;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 138-160.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43112-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 23 BP; 6 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1
RESULT 15
AAAS5810/c
ID AAAS5810 standard; DNA; 26 BP.
XX
AC AAAS5810;

XX 01-SEP-2000 (first entry)
DT Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:55.
XX
DE Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
XX WO200023112-A1.
PN
XX 27-APR-2000.
PD
XX 19-OCT-1999; 99WO-US024278.
PF
XX 19-OCT-1998; 98US-0104804P.
PR
XX (METH-) METHYLGENE INC.
PA
XX Besterman JM, Macleod AR, Siders WM;
XX
PI WPI; 2000-339532/29.
XX
DR Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Example 9; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
XX which are used in the exemplification of the present invention
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db ||||||||| ||||| |||||
26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 16
AAH43120/c
ID AAH43120 standard; DNA; 26 BP.
XX

AC AAH43120;
XX 19-SEP-2001 (first entry)
DT
XX Antisense oligo, target HDAC-2 211-236.
DE
XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
XX WO200138322-A1.
PN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-IB001881.
PF
XX 23-NOV-1999; 99US-0167035P.
PR
XX (METH-) METHYLGENE INC.
PA
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
XX WPI; 2001-432601/46.
DR
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43115-21 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db ||||||||| ||||| |||||
26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 17
AAC89535/c
ID AAC89535 standard; DNA; 26 BP.
XX
AC AAC89535;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 5.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO2000071703-A2.
PN
XX 30-NOV-2000.
PD
XX 03-MAY-2000; 2000WO-IB001252.
PF

XX 03-MAY-1999; 99US-0132287P.
XX (METH-) METHYLGENE INC.
XX Macleod AR, Li Z, Besterman JM;
XX WPI; 2001-016407/02.
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX Example 2; Page 12; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||||
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
|||||

RESULT 18
AAC89544/c
ID AAC89544 standard; DNA; 26 BP.
XX
AC AAC89544;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 14.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
XX WPI; 2001-016407/02.
XX
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX Example 1; Page 23; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting

CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 6 A; 5 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||||
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
|||||

RESULT 19
AAA55803/c
ID AAA55803 standard; DNA; 22 BP.
XX
AC AAA55803;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:46.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
XX WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;
XX
XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
XX
CC The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture

CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 22 BP; 8 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

```
Query Match      1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 166 TTGGAATTACTATTATGGACA 187
|||
Db 22 TTGGAATTACTATTATGGACA 1

RESULT 20

AAH43113/c
ID AAH43113 standard; DNA; 22 BP.

AAH43113;

DT 19-SEP-2001 (first entry)

DE Antisense oligo, target HDAC-1 166-187.

Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
fungal infections; ss.

OS Synthetic.

XX PN WO200138322-A1.

PD 31-MAY-2001.

22-NOV-2000; 2000WO-IB001881.

PR 23-NOV-1999; 99US-0167035P.

PA (METH-) METHYLGENE INC.

PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-khalil E:

DR WPI; 2001-432601/46.

PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-(benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer, PT restenosis or fungal infections.

PS Disclosure: Page 40; 147pp: English.

The sequences given in AAH43102-14 are oligonucleotides which are antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides may be used in combination with an inhibitor of histone deacetylase enzyme function, to given an improved inhibitory effect, thereby reducing the amount of inhibitor required to obtain a given inhibitory effect. Compounds containing these oligonucleotides may be used to treat cell proliferation conditions such as cancer, restenosis or psoriasis. They can also be used to treat protozoal and fungal infections

SQ Sequence 22 BP; 8 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

```
Query Match          1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred.No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 166 TTGGAATTACTATTATGGACA 187
|||
DB 22 TTGGAATTACTATTATGGACA 1

RESULT 21

AAA55808/C

AAA55808 standard; DNA; 23 BP.

AAA55808;

01-SEP-2000 (first entry)

Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:53.

Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide; modulation; inhibition; gene expression; combination therapy; p16; histone deacetylase; HDAC; thymidylate synthase; tumour suppressor; methylation; gene therapy; tumour; cytostatic; antiasthmatic; antiinflammatory; inflammation; asthma; ss.

Homo sapiens.

WC200023112-A1.

27-APR-2000.

19-OCT-1999; 99WO-US024278.

19-OCT-1998; 98US-0104804P.

(METH-) METHYLGENE INC.

Besterman JM, Macleod AR, Siders WM;

WPI: 2000-339532/29.

Inhibiting gene expression e.g. DNA methyltransferase, by treating cells with a synergistic amount of antisense oligonucleotide and protein effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy of e.g. tumors.

Disclosure: Page 29: 99pp: English:

The present invention describes a method for inhibiting the expression of a gene in a cell comprising contacting the cell with an effective synergistic amount of an antisense oligonucleotide which inhibits expression of the gene, and an effective synergistic amount of a protein effector of a product of the gene. Also described are: (1) a method for treating a disease responsive to inhibition of a gene in a mammal; (2) a method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene comprising an antisense oligonucleotide which inhibits expression of the gene in operable association with a protein effector of a gene product; and (4) a pharmaceutical composition comprising the inhibitor of (3). The methods and compositions are useful as analytical tools for transgenic studies and as therapeutic tools, e.g. as gene therapy tools for human diseases including benign and malignant tumours, inflammation or asthma. The methods, inhibitors and compositions of the invention that inhibit expression or activity of a gene or gene product may be used to treat patients having, or predisposed to developing, a disease responsive to inhibition of the gene. These may also be used to activate silenced genes to provide missing gene functions and improve a given condition.

Furthermore, the methods and compositions are useful as probes of the physiological function of a gene product in an experimental cell culture or animal system; and to evaluate the effect of inhibiting gene activity or expression. AAA55758 to AAA55842 represent oligonucleotide sequences which are used in the exemplification of the present invention.

Sequence 23 BP; 5 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 138 AAAGTCTGTTACTACTACGACGG 160
|||
Db 23 AAAGTCTGCTACTACTACGACGG 1

RESULT 22

AAH43118/c
ID AAH43118 standard; DNA; 23 BP.
XX
AC AAH43118;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-2 138-160.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
XX WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43115-21 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 23 BP; 5 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
Db 23 AAAGTCTGTACTACTACGACGG 1
|||||
23 AAAGTCTGTACTACTACGACGG 1

RESULT 23
AAA55809/c
ID AAA55809 standard; DNA; 22 BP.
XX
AC AAA55809;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:54.
XX
KW Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX

WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;
XX
DR WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
XX
CC The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 22 BP; 9 A; 4 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGACACA 187
Db 22 TTGGAATTTACTATTATGACACA 1
|||||
22 TTGGAATTTACTATTATGACACA 1

RESULT 24
AAH43119/c
ID AAH43119 standard; DNA; 22 BP.
XX
AC AAH43119;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-2 166-187.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.

XX 31-MAY-2001.
PD 22-NOV-2000; 2000WO-IB001881.
XX 23-NOV-1999; 99US-0167035P.
PF (METH-) METHYLGENE INC.
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
PI WPI; 2001-432601/46.
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
DR (benzenesulfonfylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX restenosis or fungal infections.
XX Disclosure; Page 40; 147pp; English.
XX The sequences given in AAH43115-21 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX Sequence 22 BP; 9 A; 4 C; 1 G; 8 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 166 TTGGAATTAATTACTATTATGGACA 187
Db |||||
22 TTGGAATTAATTATTATGGACA 1
RESULT 25
AAA55793/C
ID AAA55793 standard; DNA; 20 BP.
XX AAA55793;
AC
XX 01-SEP-2000 (first entry)
DT Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:36.
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
DE modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX Homo sapiens.
OS WO2000023112-A1.
XX 27-APR-2000.
XX 19-OCT-1999; 99WO-US024278.
PF 19-OCT-1998; 98US-0104804P.
XX (METH-) METHYLGENE INC.
PA Besterman JM, Macleod AR, Siders WM;
XX WPI; 2000-339532/29.
PI Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein

PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX Disclosure; Page 29; 99pp; English.
PS The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 GCTGTCTCTCCCACTCGGTTCAT 48
Db |||||
20 GCTGTCTCTCCCACTCGGTTCAT 1
RESULT 26
AAA55792/C
ID AAA55792 standard; DNA; 20 BP.
XX AAA55792;
AC
XX 01-SEP-2000 (first entry)
DT Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:35.
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
DE modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX Homo sapiens.
OS WO2000023112-A1.
XX 27-APR-2000.
XX 19-OCT-1999; 99WO-US024278.
PF 19-OCT-1998; 98US-0104804P.
XX (METH-) METHYLGENE INC.
PA Besterman JM, Macleod AR, Siders WM;
XX WPI; 2000-339532/29.
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PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
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CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
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CC inhibition of the gene. These may also be used to activate silenced genes
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CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 CCCGCTGGTCTGCTGCTC 36
DB 20 CCCGCTGGTCTGCTGCTC 1

RESULT 27
AAA55794/c
ID AAA55794 standard; DNA; 20 BP.
XX
AC AAA55794;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:37.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;
XX
DR WPI; 2000-339532/29.
XX

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PT with a synergistic amount of antisense oligonucleotide and protein
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PT of e.g. tumors.
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CC a gene in a cell comprising contacting the cell with an effective
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CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 TGTCTCCCACTCGGTCTATCC 50
DB 20 TGTCTCCCACTCGGTCTATCC 1

RESULT 28
AAA55800/c
ID AAA55800 standard; DNA; 20 BP.
XX
AC AAA55800;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:43.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;
XX
DR WPI; 2000-339532/29.
XX

XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
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CC a gene in a cell comprising contacting the cell with an effective
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CC effector of a product of the gene. Also described are: (1) a method for
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CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 29
AAA55795/c
ID AAA55795 standard; DNA; 20 BP.
XX
AC AAA55795;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:38.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;

DR WPI; 2000-339532/29.

XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX

PS Disclosure; Page 29; 99pp; English.

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CC a gene in a cell comprising contacting the cell with an effective
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CC physiological function of a gene product in an experimental cell culture
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CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX

SQ Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTG 52
|||
Db 20 TCTCCCACTCGGTCATCCTG 1

RESULT 30
AAA55796/c
ID AAA55796 standard; DNA; 20 BP.
XX
AC AAA55796;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:39.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US024278.
XX
PR 19-OCT-1998; 98US-0104804P.
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PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Macleod AR, Siders WM;

XX WPI; 2000-339532/29.
DR
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PT of e.g. tumors.
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PS Disclosure; Page 29; 99pp; English.
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CC a gene in a cell comprising contacting the cell with an effective
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CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 TCGGTCATCCTGAGAACACA 60
DB 20 TCGGTCATCCTGAGAACACA 1

RESULT 31
AAA55801/c
ID AAA55801 standard; DNA; 20 BP.
XX
AC AAA55801;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:44.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200023112-A1.
XX
PD 27-APR-2000.
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PF 19-OCT-1999; 99WO-US024278.
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PR 19-OCT-1998; 98US-0104804P.
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PA (METH-) METHYLGENE INC.
XX

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CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1585 TGCTGAGTCCTCAGGTTTC 1604
DB 20 TGCTGAGTCCTCAGGTTTC 1

RESULT 32
AAA55798/c
ID AAA55798 standard; DNA; 20 BP.
XX
AC AAA55798;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:41.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
OS Homo sapiens.
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PN WO200023112-A1.
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PD 27-APR-2000.
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PA (METH-) METHYLGENE INC.
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CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
|||||

RESULT 33
AAH43108/C
ID AAH43108 standard; DNA; 20 BP.
XX AAH43108;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 1504-1523.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
KW WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
|||||

RESULT 34
AAH43105/C
ID AAH43105 standard; DNA; 20 BP.
XX AAH43105;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 33-52.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
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PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
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KW WPI; 2001-432601/46.
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PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
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CC enzyme function, to given an improved inhibitory effect, thereby reducing
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PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
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DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
|||||

RESULT 34
AAH43105/C
ID AAH43105 standard; DNA; 20 BP.
XX AAH43105;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 33-52.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
KW WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX

CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCTCCTG 52
|||||
Db 20 TCTCCCACTCGGTCTCCTG 1

RESULT 35
AAH43102/c
ID AAH43102 standard; DNA; 20 BP.
XX
AC AAH43102;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 17-36.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer;
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
SQ The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 6 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTCTGCTCTC 36
|||||
Db 20 CCCGCTGGTCTGCTCTC 1

RESULT 36
AAH43111/c
ID AAH43111 standard; DNA; 20 BP.
XX

AC AAH43111;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 1585-1604.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer;
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
SQ The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
|||||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 37
AAH43106/c
ID AAH43106 standard; DNA; 20 BP.
XX
AC AAH43106;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 41-60.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.

XX 23-NOV-1999; 99US-0167035P.
XX (METH-) METHYLGENE INC.
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 TCGGTCATCCTGAGAACACA 60
Db 20 TCGGTCATCCTGAGAACACA 1
RESULT 38
AAH43104/c
ID AAH43104 standard; DNA; 20 BP.
XX
AC AAH43104;
XX 19-SEP-2001 (first entry)
XX Antisense oligo, target HDAC-1 31-50.
DE Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX Synthetic.
OS
XX WO200138322-A1.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-IB001881.
XX 23-NOV-1999; 99US-0167035P.
XX (METH-) METHYLGENE INC.
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides

CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 TGTCCTCCACTCGGTCTATCC 50
Db 20 TGTCCTCCACTCGGTCTATCC 1
RESULT 39
AAH43110/c
ID AAH43110 standard; DNA; 20 BP.
XX
AC AAH43110;
XX 19-SEP-2001 (first entry)
XX Antisense oligo, target HDAC-1 1565-1584.
DE Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX Synthetic.
OS
XX WO200138322-A1.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-IB001881.
XX 23-NOV-1999; 99US-0167035P.
XX (METH-) METHYLGENE INC.
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 40
AAH43103/c
ID AAH43103 standard; DNA; 20 BP.
XX
XX
AC AAH43103;
XX
XX
DT 19-SEP-2001 (first entry)
XX
XX
DE Antisense oligo, target HDAC-1 21-49.
XX
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
XX
PN WO200138322-A1.
XX
XX
PD 31-MAY-2001.
XX
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
XX
PR 23-NOV-1999; 99US-0167035P.
XX
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
XX
DR WPI; 2001-432601/46.
XX
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
XX
PS Disclosure; Page 40; 147pp; English.
XX
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
XX
SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCTCCCACTCGGTCTAT 48
DB 20 GCTGTCTCTCCCACTCGGTCTAT 1

RESULT 41
AAC89540/c
ID AAC89540 standard; DNA; 20 BP.
XX
XX
AC AAC89540;
XX
XX
DT 08-MAR-2001 (first entry)
XX
XX
DE Human HDAC-1 antisense sequence SEQ ID NO: 10.
XX
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
XX
OS Homo sapiens.
XX

PN WO200071703-A2.
XX
XX
PD 30-NOV-2000.
XX
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
XX
PR 03-MAY-1999; 99US-0132287P.
XX
XX
PA (METH-) METHYLGENE INC.
XX
XX
PI Macleod AR, Li Z, Besterman JM;
XX
XX
DR WPI; 2001-016407/02.
XX
XX
PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
PS Example 1; Page 23; 125pp; English.
XX
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
DB 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 42
AAC89531/c
ID AAC89531 standard; DNA; 20 BP.
XX
XX
AC AAC89531;
XX
XX
DT 08-MAR-2001 (first entry)
XX
XX
DE Human HDAC-1 PCR primer SEQ ID NO: 1.
XX
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200071703-A2.
XX
XX
PD 30-NOV-2000.
XX
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
XX
PR 03-MAY-1999; 99US-0132287P.
XX
XX
PA (METH-) METHYLGENE INC.
XX
XX
PI Macleod AR, Li Z, Besterman JM;
XX
XX
DR WPI; 2001-016407/02.
XX
XX
PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
PS Example 2; Page 12; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCACGTTTC 1604
 Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 43
 AAD20115/c
 ID AAD20115 standard; DNA; 20 BP.
 XX
 AC AAD20115;
 XX
 DT 03-JAN-2002 (first entry)
 XX Human histone deacetylase antisense oligonucleotide, HDAC1 AS1.
 DE
 XX Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX Homo sapiens.
 OS
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-IB000683.
 PF
 XX 24-MAR-2000; 2000US-0192151P.
 PR
 XX (METH-) METHYLGENE INC.
 PA
 XX Delorme D, Woo SH, Vaisburg A;
 PI
 XX WPI; 2001-639108/73.
 DR
 XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.
 XX
 CC The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC1 AS1 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC1 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCACGTTTC 1604
 Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 44
 AAD20116/c
 ID AAD20116 standard; DNA; 20 BP.
 XX
 AC AAD20116;
 XX
 DT 03-JAN-2002 (first entry)
 XX Human histone deacetylase antisense oligonucleotide, HDAC1 AS2.
 DE
 XX Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX Homo sapiens.
 OS
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-IB000683.
 PF
 XX 24-MAR-2000; 2000US-0192151P.
 PR
 XX (METH-) METHYLGENE INC.
 PA
 XX Delorme D, Woo SH, Vaisburg A;
 PI
 XX WPI; 2001-639108/73.
 DR
 XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.
 XX
 CC The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC1 AS1 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC1 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCACGTTTC 1604
 Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 44
 AAD20116/c
 ID AAD20116 standard; DNA; 20 BP.
 XX
 AC AAD20116;
 XX
 DT 03-JAN-2002 (first entry)
 XX Human histone deacetylase antisense oligonucleotide, HDAC1 AS2.
 DE
 XX Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX Homo sapiens.
 OS
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-IB000683.
 PF
 XX 24-MAR-2000; 2000US-0192151P.
 PR
 XX (METH-) METHYLGENE INC.
 PA
 XX Delorme D, Woo SH, Vaisburg A;
 PI
 XX WPI; 2001-639108/73.
 DR
 XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.
 XX
 CC The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC1 AS2 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC1 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
 Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 45
 AAD40908/c
 ID AAD40908 standard; DNA; 20 BP.
 XX
 AC AAD40908;
 XX
 DT 30-OCT-2002 (first entry)
 XX Human HDAC1 antisense oligonucleotide ISIS #123689.

Human HDAC1 antisense oligonucleotide ISIS #123689.
 XX Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.

OS XX Synthetic.

FH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 1..4

FT /*tag= d

FT /mod_base= m5c

FT modified_base 9..10

FT /*tag= e

FT /mod_base= m5c

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 20

FT /*tag= f

FT /mod_base= m5c

XX WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone

XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.

XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

XX infection.

XX Claim 3; Page 93; 120pp; English.

XX The present invention relates to antisense compounds, compositions and

XX methods for modulating the expression of Histone deacetylase 1 (HDAl).

XX Sequences of the invention are useful for inhibiting the expression of

XX HDAl in cells or tissues and for treating an animal having a disease or

XX condition associated with HDAl e.g., hyperproliferative condition, which

XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition

XX resulting from a viral infection. Antisense compounds either alone or in

XX combination with other antisense compounds or therapeutics can be used as

XX tools in differential and/or combinatorial analyses to elucidate the

XX expression patterns of a portion or the entire complement of genes

XX expressed within cells and tissues. They are commonly used as research

XX reagents and diagnostics. They may also be useful prophylactically such

XX as to prevent or delay infection, inflammation or tumour formation. The

XX present DNA sequence is an antisense oligonucleotide targeted to human

XX HDAl DNA

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCAGGAAGTGGGG 738

|||||

Db 20 GTACTTCCAGGAAGTGGGG 1

RESULT 46

AAD40910/c

ID AAD40910 standard; DNA; 20 BP.

XX

AC AAD40910;

XX

DT 30-OCT-2002 (first entry)

XX

DE Human HDAl antisense oligonucleotide ISIS #123691.

XX

XW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;

XW viral infection; prophylactic; inflammation; phosphorothioate backbone;

XW tumour; antisense; cytostatic; virucide; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 2..4

FT /*tag= d

FT /mod_base= m5c

FT modified_base 11..14

FT /*tag= e

FT /mod_base= m5c

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 19..20

FT /*tag= f

FT /mod_base= m5c

XX

WO200250244-A2.

XX

PD 27-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-US046518.

XX

PR 19-DEC-2000; 2000US-00745167.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Wyatt JR;

XX

DR WPI; 2002-519880/55.

XX

PT Antisense compounds targeted against polynucleotides encoding Histone

PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.

PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

PT infection.

XX

PS Claim 3; Page 93; 120pp; English.

XX

CC The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of Histone deacetylase 1 (HDAl).

CC Sequences of the invention are useful for inhibiting the expression of

CC HDAl in cells or tissues and for treating an animal having a disease or

CC condition associated with HDAl e.g., hyperproliferative condition, which

CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition

CC resulting from a viral infection. Antisense compounds either alone or in

CC combination with other antisense compounds or therapeutics can be used as

CC tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes

CC expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such

CC as to prevent or delay infection, inflammation or tumour formation. The

CC present DNA sequence is an antisense oligonucleotide targeted to human

CC HDAl DNA

XX

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCAGGAAGTGGGG 738

|||||

Db 20 GTACTTCCAGGAAGTGGGG 1

CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 GGAAGTGGGGACCTACGGGA 748
Db 20 GGAAGTGGGGACCTACGGGA 1
RESULT 47
AAD40912/c
ID AAD40912 standard; DNA; 20 BP.
XX
AC AAD40912;
XX
AC AAD40912;
DT 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123693.
DE
DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /tag= d
FT /mod_base= m5c
FT modified_base 5..7
FT /tag= e
FT /mod_base= m5c
FT modified_base 10
FT /tag= f
FT /mod_base= m5c
FT modified_base 12
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base 17
FT /tag= h
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
PF
XX 19-DEC-2000; 2000US-00745167.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
PI
XX

DR WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX Claim 3; Page 93; 120pp; English.
PS The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 788 CCCGCTCCGAGACGGGATTG 807
Db 20 CCCGCTCCGAGACGGGATTG 1
RESULT 48
AAD40913/c
ID AAD40913 standard; DNA; 20 BP.
XX
AC AAD40913;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123694.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6..7
FT /tag= d
FT /mod_base= m5c
FT modified_base 9
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base 16
FT /note= "2'-methoxyethyl residues"

FT FT /*tag= f /mod_base= m5c
FT modified_base 18
FT /*tag= g /mod_base= m5c
XX
PN WO200250244-A2.
XX
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCCTATGAGGCATT 830
Db 20 ACGAGTCCTATGAGGCATT 1

RESULT 49
AAD40926/c
ID AAD40926 standard; DNA; 20 BP.
XX
AC AAD40926;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123707.
XX
XW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
XW viral infection; prophylactic; inflammation; phosphorothioate backbone;
XW tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20

FT FT /*tag= a /mod_base= OTHER
FT modified_base 1. .5 /note= "Phosphorothioate backbone"
FT /*tag= b /mod_base= OTHER
FT modified_base 6 /note= "2'-methoxyethyl residues"
FT /*tag= d /mod_base= m5c
FT modified_base 9
FT /*tag= e /mod_base= m5c
FT modified_base 11. .12
FT /*tag= f /mod_base= m5c
FT modified_base 16. .20
FT /*tag= c /mod_base= OTHER
FT modified_base 18 /note= "2'-methoxyethyl residues"
FT /*tag= g /mod_base= m5c
FT modified_base 20
FT /*tag= h /mod_base= m5c
FT
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAGATCAA 1198
Db 20 GAGTACCTGGAGAGATCAA 1

CC methods for modulating the expression of Histone deacetylase 1 (HDAl) .
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1509 GAGGAGAAGCCAGAGCCAA 1528
Db 20 GAGGAGAAGCCAGAGCCAA 1

RESULT 51

AAD40893/c
ID AAD40893 standard; DNA; 20 BP.

XX AAD40893;

AC AAD40893;

XX 30-OCT-2002 (first entry)

DE Human HDAl antisense oligonucleotide ISIS #123674.

XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/tag= a
	/mod_base= OTHER
	/note= "Phosphorothioate backbone"
modified_base	1..5
	/tag= b
	/mod_base= OTHER
	/note= "2'-methoxyethyl residues"
modified_base	1..2
	/tag= d
	/mod_base= m5c
modified_base	4
	/tag= e
	/mod_base= m5c
modified_base	7
	/tag= f
	/mod_base= m5c
modified_base	13
	/tag= g
	/mod_base= m5c
modified_base	16..20
	/tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl residues"

WO200250244-A2.

27-JUN-2002.

RESULT 50

AAD40935/c

ID AAD40935 standard; DNA; 20 BP.

XX AAD40935;

AC AAD40935;

XX 30-OCT-2002 (first entry)

DE Human HDAl antisense oligonucleotide ISIS #123716.
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.
OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/tag= a
	/mod_base= OTHER
	/note= "Phosphorothioate backbone"
modified_base	1..5
	/tag= b
	/mod_base= OTHER
	/note= "2'-methoxyethyl residues"
modified_base	5
	/tag= d
	/mod_base= m5c
modified_base	8
	/tag= e
	/mod_base= m5c
modified_base	12
	/tag= f
	/mod_base= m5c
modified_base	15
	/tag= g
	/mod_base= m5c
modified_base	16..20
	/tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl residues"
modified_base	17..18
	/tag= h
	/mod_base= m5c
modified_base	20
	/tag= i
	/mod_base= m5c

WO200250244-A2.

27-JUN-2002.

07-DEC-2001; 2001WO-US046518.

19-DEC-2000; 2000US-00745167.

(ISIS-) ISIS PHARM INC.

Monia BP, Wyatt JR;

WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.

XX Claim 3; Page 94; 120pp; English.

PS The present invention relates to antisense compounds, compositions and

CC

PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCCAATGCTGAGG 297
Db 20 TCACAAAGCCCAATGCTGAGG 1

RESULT 52
AAD40887/c
ID AAD40887 standard; DNA; 20 BP.
XX
AC AAD40887;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123668.
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 9
FT /tag= d
FT /mod_base= m5c

FT modified_base 13
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17..18
FT /tag= f
FT /mod_base= m5c
FT modified_base 20
FT /tag= g
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
DR Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
PT
XX Claim 3; Page 93; 120pp; English.
PS
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCTGTTACTACT 153
Db 20 GAGGAAAGTCTGTTACTACT 1

RESULT 53
AAD40892/c
ID AAD40892 standard; DNA; 20 BP.
XX
AC AAD40892;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123673.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= m5c
FT modified_base 8
FT /*tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT modified_base 19
FT /*tag= f
FT /mod_base= m5c
XX
XX WO200250244-A2.
PN
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 2 A; 3 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCTCACAAAGCCAATGC 292

Db 20 CGCCTCACAAAGCCAATGC 1
RESULT 54
AAD40897/c
ID AAD40897 standard; DNA; 20 BP.
XX
XX AAD40897;
XX
DT 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123678.
DE
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /*tag= d
FT /mod_base= m5c
FT modified_base 3
FT /*tag= e
FT /mod_base= m5c
FT modified_base 6
FT /*tag= f
FT /mod_base= m5c
FT modified_base 9
FT /*tag= g
FT /mod_base= m5c
FT modified_base 12
FT /*tag= h
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16
FT /*tag= i
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.

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CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDA1 DNA
XX SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 369 TACAGCAAGCAGATGCAGAG 388
Db 20 TACAGCAAGCAGATGCAGAG 1

RESULT 55
AAD40925/c
ID AAD40925 standard; DNA; 20 BP.
XX AC AAD40925;
XX 30-OCT-2002 (first entry)
XX Human HDA1 antisense oligonucleotide ISIS #123706.
XX Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.

XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2
FT /tag= d
FT /mod_base= m5c
FT modified_base 4..5
FT /tag= e
FT /mod_base= m5c
FT modified_base 11
FT /tag= f
FT /mod_base= m5c
FT modified_base 13
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= h
FT /mod_base= m5c

XX WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.

XX Claim 3; Page 94; 120pp; English.
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDA1 DNA
XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1172 CACGAATGAGTACCTGGAGA 1191
Db 20 CACGAATGAGTACCTGGAGA 1
RESULT 56
AAD40932/c
ID AAD40932 standard; DNA; 20 BP.
XX AC AAD40932;
XX 30-OCT-2002 (first entry)
XX Human HDA1 antisense oligonucleotide ISIS #123713.
XX Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b

FT /mod_base= OTHER
FT modified_base 5 /note= "2'-methoxyethyl residues"
FT /tag= d
FT /mod_base= m5c
FT modified_base 9 /tag= e
FT /mod_base= m5c
FT modified_base 11 /tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base 17 /tag= g
FT /mod_base= m5c
FT modified_base 20 /tag= h
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
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CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAGAGAAAGACCC 1468
|||||
Db 20 GATGAAAAGAGAAAGACCC 1

RESULT 57
AAD40937/c
ID AAD40937 standard; DNA; 20 BP.

XX AAD40937;
AC
XX 30-OCT-2002 (first entry)
DT
XX
DE Human HDA1 antisense oligonucleotide ISIS #123718.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5 /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 5..6 /tag= d
FT /mod_base= m5c
FT modified_base 10 /tag= e
FT /mod_base= m5c
FT modified_base 14..15 /tag= f
FT /mod_base= m5c
FT modified_base 16..20 /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 18 /tag= g
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
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XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
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PS Claim 3; Page 94; 120pp; English.
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CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX

CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1548 AAGTTGGCCTGAATGGACCT 1567
Db 20 AAGTTGGCCTGAATGGACCT 1
RESULT 58
AAD40938/c
ID AAD40938 standard; DNA; 20 BP.
XX
AC AAD40938;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123719.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
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FT /*tag= d
FT /mod_base= m5c
FT modified_base 12
FT /*tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX

CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1
RESULT 59
AAD40886/c
ID AAD40886 standard; DNA; 20 BP.
XX
AC AAD40886;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123667.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2
FT /*tag= d
FT /mod_base= m5c
FT modified_base 5
FT /*tag= e
FT /mod_base= m5c
FT modified_base 7..8
FT /*tag= f
FT /mod_base= m5c
FT modified_base 11
FT /*tag= g
FT /mod_base= m5c
FT modified_base 15
FT /*tag= h
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17

FT FT /*tag= i /mod_base= m5c
FT modified_base 19..20
FT /*tag= j /mod_base= m5c
FT XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GGCAGCAAGATGGCGCAGA 120
Db 20 GGCAGCAAGATGGCGCAGA 1

RESULT 60
AAD40894/c
ID AAD40894 standard; DNA; 20 BP.
XX
AC AAD40894;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #1233675.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20

FT FT /*tag= a /mod_base= OTHER
FT modified_base 1..5 /note= "Phosphorothioate backbone"
FT /*tag= b /mod_base= OTHER
FT modified_base 1 /note= "2'-methoxyethyl residues"
FT /*tag= d /mod_base= m5c
FT modified_base 4 /mod_base= m5c
FT /*tag= e /mod_base= m5c
FT modified_base 6..7 /mod_base= m5c
FT /*tag= f /mod_base= m5c
FT modified_base 9 /mod_base= m5c
FT /*tag= g /mod_base= m5c
FT modified_base 12 /mod_base= m5c
FT /*tag= h /mod_base= m5c
FT modified_base 16..20 /mod_base= m5c
FT /*tag= c /mod_base= OTHER
FT modified_base 18 /note= "2'-methoxyethyl residues"
FT /*tag= i /mod_base= m5c

WO200250244-A2.
27-JUN-2002.
07-DEC-2001; 2001WO-US046518.
19-DEC-2000; 2000US-00745167.
(ISIS-) ISIS PHARM INC.
Monia BP, Wyatt JR;
WPI; 2002-519880/55.
Antisense compounds targeted against polynucleotides encoding Histone
deacetylase 1 useful for treating hyperproliferative conditions, e.g.
cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
infection.
Claim 3; Page 93; 120pp; English.
The present invention relates to antisense compounds, compositions and
methods for modulating the expression of Histone deacetylase 1 (HDAl).
Sequences of the invention are useful for inhibiting the expression of
HDAl in cells or tissues and for treating an animal having a disease or
condition associated with HDAl e.g., hyperproliferative condition, which
is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
resulting from a viral infection. Antisense compounds either alone or in
combination with other antisense compounds or therapeutics can be used as
tools in differential and/or combinatorial analyses to elucidate the
expression patterns of a portion or the entire complement of genes
expressed within cells and tissues. They are commonly used as research
reagents and diagnostics. They may also be useful prophylactically such
as to prevent or delay infection, inflammation or tumour formation. The
present DNA sequence is an antisense oligonucleotide targetted to human
HDAl DNA
Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Claim 3; Page 93; 120pp; English.
The present invention relates to antisense compounds, compositions and
methods for modulating the expression of Histone deacetylase 1 (HDAl).
Sequences of the invention are useful for inhibiting the expression of
HDAl in cells or tissues and for treating an animal having a disease or
condition associated with HDAl e.g., hyperproliferative condition, which
is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
resulting from a viral infection. Antisense compounds either alone or in
combination with other antisense compounds or therapeutics can be used as
tools in differential and/or combinatorial analyses to elucidate the
expression patterns of a portion or the entire complement of genes
expressed within cells and tissues. They are commonly used as research
reagents and diagnostics. They may also be useful prophylactically such
as to prevent or delay infection, inflammation or tumour formation. The
present DNA sequence is an antisense oligonucleotide targetted to human
HDAl DNA
Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Claim 3; Page 93; 120pp; English.

The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl). Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAl DNA

Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 GACTGTCCAGTATTCGATGG 424
Db 20 GACTGTCCAGTATTCGATGG 1

RESULT 62
AAD40919/c
ID AAD40919 standard; DNA; 20 BP.
XX
AC AAD40919;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123700.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
XX Synthetic.

Key Location/Qualifiers
modified_base 1..20
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/note= "Phosphorothioate backbone"
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/note= "2'-methoxyethyl residues"
modified_base 10
/*tag= d
/mod_base= m5c
modified_base 13..14
/*tag= e
/mod_base= m5c
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl residues"
modified_base 18..19
/*tag= f
/mod_base= m5c

WO200250244-A2.
27-JUN-2002.

283 AAGCCAATGCTGAGGATG 302
20 AAGCCAATGCTGAGGATG 1

RESULT 61
AAD40898/c
ID AAD40898 standard; DNA; 20 BP.
XX
AC AAD40898;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123679.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
XX Synthetic.

Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
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/note= "2'-methoxyethyl residues"
modified_base 1
/*tag= d
/mod_base= m5c
modified_base 2
/*tag= e
/mod_base= m5c
modified_base 5
/*tag= f
/mod_base= m5c
modified_base 11
/*tag= g
/mod_base= m5c
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl residues"
modified_base 16
/*tag= h
/mod_base= m5c
modified_base 20
/*tag= i
/mod_base= m5c

WO200250244-A2.
27-JUN-2002.
07-DEC-2001; 2001WO-US046518.
19-DEC-2000; 2000US-00745167.
(ISIS-) ISIS PHARM INC.
Monia BP, Wyatt JR;
WPI; 2002-519880/55.
Antisense compounds targetted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.

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PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
DR
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
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PT infection.
XX
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CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
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CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 918 CGGTTAGTGTGCTTCAATCT 937
Db 20 CGGTTAGTGTGCTTCAATCT 1
RESULT 63
AAD40889/c
ID AAD40889 standard; DNA; 20 BP.
XX
AC AAD40889;
XX
XX 30-OCT-2002 (first entry)
DT
XX Human HDAl antisense oligonucleotide ISIS #123670.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
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FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6..7
FT /*tag= d
FT /mod_base= m5c
FT
PF 07-DEC-2001; 2001WO-US046518.
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PR 19-DEC-2000; 2000US-00745167.
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PA (ISIS-) ISIS PHARM INC.
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PI Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
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XX
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 918 CGGTTAGTGTGCTTCAATCT 937
Db 20 CGGTTAGTGTGCTTCAATCT 1
RESULT 64
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ID AAD40921 standard; DNA; 20 BP.
XX
AC AAD40921;
XX
XX 30-OCT-2002 (first entry)
DT
XX Human HDAl antisense oligonucleotide ISIS #123702.
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KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
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XX WO200250244-A2.
PN
XX 27-JUN-2002.
PD
XX
XX 07-DEC-2001; 2001WO-US046518.
PF
XX
XX 19-DEC-2000; 2000US-00745167.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
DR
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 GCTGCTCAACTATGGTCTCT 252
Db 20 GCTGCTCAACTATGGTCTCT 1
RESULT 64
AAD40921/c
ID AAD40921 standard; DNA; 20 BP.
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AC AAD40921;
XX
XX 30-OCT-2002 (first entry)
DT
XX Human HDAl antisense oligonucleotide ISIS #123702.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
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OS	Synthetic.
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FT	/note= "2'-methoxyethyl residues"
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PN	WO200250244-A2.
XX	
PD	27-JUN-2002.
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PF	07-DEC-2001; 2001WO-US046518.
XX	
PR	19-DEC-2000; 2000US-00745167.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Monia BP, Wyatt JR;
XX	
DR	WPI; 2002-519880/55.
XX	
PT	Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
PT	
PS	Claim 3; Page 94; 120pp; English.
XX	
CC	The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC	Sequences of the invention are useful for inhibiting the expression of HDAL in cells or tissues and for treating an animal having a disease or condition associated with HDAL e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAL DNA
XX	
SO	Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Sequence 20 BP: 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Claim 3: Page 93; 120pp; English.

The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAC1). Sequences of the invention are useful for inhibiting the expression of HDAC1 in cells or tissues and for treating an animal having a disease or condition associated with HDAC1 e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAC1 DNA

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20: Conservative 0; Mismatches 0; Indels

QY 663 GAGGCCCTTCTACACCAACCGGA 682
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Db 20 GAGGCCCTTCTACACCAACCGGA 1

RESULT 67

ID AAD40911 standard; DNA; 20 BP.

AC AAD40911;

DT 30-OCT-2002 (first entry)

Human HDAl antisense oligonucleotide ISIS #123692.

AA	Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW	Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW	viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW	tumour; antisense; cytostatic; virucide; ss.

OS Homo sapiens.
OS Synthetic.

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FF / **tag= b

XX KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX OS Homo sapiens.
OS Synthetic.
XX FT Key Location/Qualifiers
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XX WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX Claim 3; Page 93; 120pp; English.
XX The present invention relates to antisense compounds, compositions and
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CC condition associated with HDAl e.g., hyperproliferative condition, which
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CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX SQ Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
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CC combination with other antisense compounds or therapeutics can be used as
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CC expression patterns of a portion or the entire complement of genes
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CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX SQ Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 20 AGTATTATGCTGTTAACTAC 1
RESULT 68
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XX AAD40888;
AC AAD40888;
XX 30-OCT-2002 (first entry)
DT Human HDAl antisense oligonucleotide ISIS #123669.
XX DE

QY 228 AATTGCTGCTCAACTATGG 247
Db 20 AATTGCTGCTCAACTATGG 1

RESULT 69
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ID AAD40896 standard; DNA; 20 BP.
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AC AAD40896;
XX 30-OCT-2002 (first entry)
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DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
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OS Synthetic.
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XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
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CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAl DNA
XX

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 TGAGGAGATGACCAAGTACC 312
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AC AAD40915;
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DT 30-OCT-2002 (first entry)
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DE Human HDAl antisense oligonucleotide ISIS #123696.
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KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
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OS Homo sapiens.
OS Synthetic.
XX

Key Location/Qualifiers
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PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl). Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAl DNA
XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 20 GTCCAAAGTAATGGAGATGT 1
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AC AAD40924;
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DT 30-OCT-2002 (first entry)
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DE Human HDAl antisense oligonucleotide ISIS #123705.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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XX 19-DEC-2000; 2000US-00745167.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
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XX Monia BP, Wyatt JR;
PI
XX
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
PT
PT
PT
PT
XX
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XX
CC The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl). Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAl DNA
XX
SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC AAD40914;
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DT 30-OCT-2002 (first entry)
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XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
KW

XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key
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XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
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XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targetted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GTCATGTCCAAAGTAATGGA 859
Db |||||
20 GTCATGTCCAAAGTAATGGA 1
RESULT 73
AAD40930/c
ID AAD40930 standard; DNA; 20 BP.
XX
XX
AC AAD40930;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123711.
DE
XX
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 3
FT /tag= d
FT /mod_base= m5c
FT modified_base 5
FT /tag= e
FT /mod_base= m5c
FT modified_base 8..9
FT /tag= f
FT /mod_base= m5c
FT modified_base 11
FT /tag= g
FT /mod_base= m5c
FT modified_base 13
FT /tag= h
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= i
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.

PS Claim 3; Page 94; 120pp; English.

XX The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl).

CC Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAl DNA

XX Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCTGTGAGGAAGAGTT 1369
|||||
Db 20 ATTGCTGTGAGGAAGAGTT 1

RESULT 74
AAD40933/c
ID AAD40933 standard; DNA; 20 BP.
XX AAD40933;
AC AAD40933;
XX 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123714.
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..20 /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2
FT /tag= d
FT /mod_base= m5c
FT modified_base 5
FT /tag= e
FT /mod_base= m5c
FT modified_base 7..8
FT /tag= f
FT /mod_base= m5c
FT modified_base 10..11
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 20
FT /tag= h

FT XX WO200250244-A2. /mod_base= m5c
PN 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
DR Antisense compounds targetted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
XX Example 15; Page 94; 120pp; English.
PS The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl). Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targetted to human HDAl DNA

XX Sequence 20 BP; 0 A; 7 C; 3 G; 10 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAACCAAGGAGGAGC 1518
|||||
Db 20 GAAACCAAGGAGGAGC 1

RESULT 75
AAD40907/c
ID AAD40907 standard; DNA; 20 BP.
XX AAD40907;
AC AAD40907;
XX 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123688.
DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition; viral infection; prophylactic; inflammation; phosphorothioate backbone; tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..20 /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5

CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAAGACGACCCCTGAC 1316
Db 20 AGGACGAAGACGACCCCTGAC 1

RESULT 77
AAD40936/C
ID AAD40936 standard; DNA; 20 BP.
XX
AC AAD40936;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123717.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
FT modified_base 1..5 /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl residues"
FT modified_base 1..4 /*tag= d
FT /*mod_base= m5c
FT modified_base 10 /*tag= e
FT /*mod_base= m5c
FT modified_base 13 /*tag= f
FT /*mod_base= m5c
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT modified_base 17 /*note= "2'-methoxyethyl residues"
FT modified_base 17 /*tag= g
FT /*mod_base= m5c
FT modified_base 20 /*tag= h
FT /*mod_base= m5c
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAAGCCAGAGCCCAAGGGG 1533
Db 20 GAAGCCAGAGCCCAAGGGG 1

RESULT 78
AAD40905/C
ID AAD40905 standard; DNA; 20 BP.
XX
AC AAD40905;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123686.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
FT modified_base 1..5 /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl residues"
FT modified_base 8..9 /*tag= d
FT /*mod_base= m5c
FT modified_base 11 /*tag= e
FT /*mod_base= m5c
FT modified_base 14..15 /*tag= f
FT /*mod_base= m5c
FT modified_base 16..20

OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone"
FT	modified_base
FT	1..5
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl residues"
FT	7
FT	/*tag= d
FT	/mod_base= m5c
FT	9
FT	/*tag= e
FT	/mod_base= m5c
FT	14
FT	/*tag= f
FT	/mod_base= m5c
FT	16..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl residues"
FT	20
FT	/*tag= g
FT	/mod_base= m5c
XX	
PN	WO200250244-A2.
XX	
PD	27-JUN-2002.
XX	
PF	07-DEC-2001; 2001WO-US046518.
XX	
PR	19-DEC-2000; 2000US-00745167.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Monia BP, Wyatt JR;
XX	
DR	WPI; 2002-519880/55.
XX	
PT	Antisense compounds targeted against polynucleotide deacetylase 1 useful for treating hyperproliferative cancer of hematopoietic, lymphoid, myeloid or B-cell infection.
PS	Claim 3; Page 94; 120pp; English.
CC	The present invention relates to antisense compound methods for modulating the expression of Histone d
CC	Sequences of the invention are useful for inhibiting HDAl in cells or tissues and for treating an animal condition associated with HDAl e.g., hyperproliferative cancer of haematopoietic, lymphoid, myeloid or resulting from a viral infection. Antisense compounds combination with other antisense compounds or their tools in differential and/or combinatorial analyses expressed within cells and tissues. They are common reagents and diagnostics. They may also be useful as to prevent or delay infection, inflammation or present DNA sequence is an antisense oligonucleotide HDAl DNA
XX	
SQ	Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
	Query Match 1.2%; Score 20; DB 1; Len
	Best Local Similarity 100.0%; Pred. No. 26;
	Matches 20; Conservative 0; Mismatches 0;
OY	1308 GACCCTGACAGCGCATCTC 1327

Db 20 GACCTGACAGCGCATCTC 1

RESULT 80

AAD40904/c

ID AAD40904 standard; DNA; 20 BP.

XX

AC AAD40904;

XX

DT 30-OCT-2002 (first entry)

XX

DE Human HDA1 antisense oligonucleotide ISIS #123685.

XX

KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;

KW tumour; antisense; cytostatic; virucide; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 2

FT /tag= d

FT /mod_base= m5c

FT modified_base 7..8

FT /tag= e

FT /mod_base= m5c

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 16..17

FT /tag= f

FT /mod_base= m5c

FT

XX

PN WO200250244-A2.

XX

PD 27-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-US046518.

XX

PR 19-DEC-2000; 2000US-00745167.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Wyatt JR;

XX

DR WPI; 2002-519880/55.

XX

PT Antisense compounds targeted against polynucleotides encoding Histone

PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.

PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

PT infection.

XX

PS Claim 3; Page 93; 120pp; English.

XX

CC The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of Histone deacetylase 1 (HDAL).

CC Sequences of the invention are useful for inhibiting the expression of

CC HDAL in cells or tissues and for treating an animal having a disease or

CC condition associated with HDAL e.g., hyperproliferative condition, which

CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

CC resulting from a viral infection. Antisense compounds either alone or in

CC combination with other antisense compounds or therapeutics can be used as

CC tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes

CC expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such

CC as to prevent or delay infection, inflammation or tumour formation. The

CC present DNA sequence is an antisense oligonucleotide targetted to human

CC HDAL DNA

XX

SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGGCCATCCTGGAACTGC 600

Db 20 CTTGGCCATCCTGGAACTGC 1

RESULT 81

AAD40917/c

ID AAD40917 standard; DNA; 20 BP.

XX

AC AAD40917;

XX

DT 30-OCT-2002 (first entry)

XX

DE Human HDA1 antisense oligonucleotide ISIS #123698.

XX

KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;

KW tumour; antisense; cytostatic; virucide; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 1

FT /tag= d

FT /mod_base= m5c

FT modified_base 3

FT /tag= e

FT /mod_base= m5c

FT modified_base 5

FT /tag= f

FT /mod_base= m5c

FT modified_base 10

FT /tag= g

FT /mod_base= m5c

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 16

FT /tag= h

FT /mod_base= m5c

FT modified_base 19

FT /tag= i

FT /mod_base= m5c

XX

PN WO200250244-A2.

XX

PD 27-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-US046518.

XX

PR 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
PS
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 AGATGTTCCAGCCTAGTGCG 878
DB 20 AGATGTTCCAGCCTAGTGCG 1

RESULT 82
AAD40923/c
ID AAD40923 standard; DNA; 20 BP.
XX
AC AAD40923;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123704.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 5..6
FT /*tag= d
FT /mod_base= m5c
FT modified_base 11..12
FT /*tag= e

FT modified_base 14
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /*tag= g
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
XX 27-JUN-2002.
PD
XX 07-DEC-2001; 2001WO-US046518.
PF
XX 19-DEC-2000; 2000US-00745167.
PR
XX (ISIS-) ISIS PHARM INC.
PA Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
PS
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGGCCCTGGATAC 1075
DB 20 ACAGCTGTGGCCCTGGATAC 1

RESULT 83
AAD40909/c
ID AAD40909 standard; DNA; 20 BP.
XX
AC AAD40909;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123690.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

XX	AD40931/c
XX	ID AD40931 standard; DNA; 20 BP.
XX	AC AAD40931;
XX	DT 30-OCT-2002 (first entry)
XX	DE Human HDA1 antisense oligonucleotide ISIS #123712.
XX	Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
XX	viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX	tumour; antisense; cytostatic; virucide; ss.
XX	Homo sapiens.
XX	Synthetic.
XX	Key
XX	Location/Qualifiers
XX	modified_base
XX	1. .20
XX	/*tag= a
XX	/mod_base= OTHER
XX	/note= "Phosphorothioate backbone"
XX	modified_base
XX	1. .5
XX	/*tag= b
XX	/mod_base= OTHER
XX	/note= "2'-methoxyethyl residues"
XX	modified_base
XX	1. .4
XX	/*tag= d
XX	/mod_base= m5c
XX	modified_base
XX	6
XX	/*tag= e
XX	/mod_base= m5c
XX	modified_base
XX	8
XX	/*tag= f
XX	/mod_base= m5c
XX	modified_base
XX	9. .10
XX	/*tag= g
XX	/mod_base= m5c
XX	modified_base
XX	12. .13
XX	/*tag= h
XX	/mod_base= m5c
XX	modified_base
XX	15
XX	/*tag= i
XX	/mod_base= m5c
XX	modified_base
XX	16. .20
XX	/*tag= c
XX	/mod_base= OTHER
XX	/note= "2'-methoxyethyl residues"
XX	modified_base
XX	18
XX	/*tag= j
XX	/mod_base= m5c
XX	WO200250244-A2.
XX	27-JUN-2002.
XX	07-DEC-2001; 2001WO-US046518.
XX	19-DEC-2000; 2000US-00745167.
XX	(ISIS-) ISIS PHARM INC.
XX	Monia BP, Wyatt JR;
XX	WPI; 2002-519880/55.
XX	Antisense compounds targeted against polynucleotides encoding Histone
XX	deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX	cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX	infection.
XX	Claim 3; Page 94; 120pp; English.
XX	The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 1 A; 12 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1378 CTGAAGAGGAGGGAGAGGGG 1397
Db 20 CTGAAGAGGAGGGAGAGGGG 1

RESULT 85
AAD40891/c
ID AAD40891 standard; DNA; 20 BP.
XX
AC AAD40891;
XX 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123672.
DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 7
FT /tag= d
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16..17
FT /tag= e
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX

PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.

XX Claim 3; Page 93; 120pp; English.

XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX

SQ Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGGTCTCTACCGAAAAAT 262
Db 20 TATGGTCTCTACCGAAAAAT 1

RESULT 86

AAD40900/c
ID AAD40900 standard; DNA; 20 BP.

XX AAD40900;

XX 30-OCT-2002 (first entry)

XX Human HDAl antisense oligonucleotide ISIS #123681.

XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2..3
FT /tag= d
FT /mod_base= m5c
FT modified_base 6
FT /tag= e
FT /mod_base= m5c
FT modified_base 9
FT /tag= f
FT /mod_base= m5c

FT modified_base 12
FT /*tag= g
FT /mod_base= m5c
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 CTTAATAAGCAGCAGACGGA 499
DB 20 CTTAATAAGCAGCAGACGGA 1

RESULT 87
AAD40890/c
ID AAD40890 standard; DNA; 20 BP.
XX
AC AAD40890;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123671.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2
FT /*tag= d
FT /mod_base= m5c
FT modified_base 11. .12
FT /*tag= e
FT /mod_base= m5c
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDA1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDA1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDA1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDA1 DNA
XX
SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGGTCTCTACCGA 257
DB 20 TCAACTATGGTCTCTACCGA 1

RESULT 88
AAD40916/c
ID AAD40916 standard; DNA; 20 BP.
XX
AC AAD40916;

30-OCT-2002 (first entry)
Human HDAl antisense oligonucleotide ISIS #123697.
Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
viral infection; prophylactic; inflammation; phosphorothioate backbone;
tumour; antisense; cytostatic; virucide; ss.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
modified_base 1..5
/*tag= b
/mod_base= OTHER
/note= "2'-methoxyethyl residues"
modified_base 1
/*tag= d
/mod_base= m5c
modified_base 7
/*tag= e
/mod_base= m5c
modified_base 10
/*tag= f
/mod_base= m5c
modified_base 12..13
/*tag= g
/mod_base= m5c
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl residues"
modified_base 18
/*tag= h
/mod_base= m5c

WO200250244-A2.

27-JUN-2002.

07-DEC-2001; 2001WO-US046518.

19-DEC-2000; 2000US-00745167.

(ISIS-) ISIS PHARM INC.

Monia BP, Wyatt JR;

WPI; 2002-519880/55.

Antisense compounds targeted against polynucleotides encoding Histone
deacetylase 1 useful for treating hyperproliferative conditions, e.g.
cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
infection.

Claim 3; Page 94; 120pp; English.

The present invention relates to antisense compounds, compositions and
methods for modulating the expression of Histone deacetylase 1 (HDAl).
Sequences of the invention are useful for inhibiting the expression of
HDAl in cells or tissues and for treating an animal having a disease or
condition associated with HDAl e.g., hyperproliferative condition, which
is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
resulting from a viral infection. Antisense compounds either alone or in
combination with other antisense compounds or therapeutics can be used as
tools in differential and/or combinatorial analyses to elucidate the
expression patterns of a portion or the entire complement of genes
expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA

SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 AAGTAATGGAGATGTCCAG 869

Db 20 AAGTAATGGAGATGTCCAG 1

RESULT 89

AAD40922/c

ID AAD40922 standard; DNA; 20 BP.

XX AAD40922;

DT 30-OCT-2002 (first entry)

DE Human HDAl antisense oligonucleotide ISIS #123703.

XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

modified_base 1..20

/*tag= a

/mod_base= OTHER

/note= "Phosphorothioate backbone"

modified_base 1..5

/*tag= b

/mod_base= OTHER

/note= "2'-methoxyethyl residues"

modified_base 11..12

/*tag= d

/mod_base= m5c

modified_base 14..15

/*tag= e

/mod_base= m5c

modified_base 16..20

/*tag= c

/mod_base= OTHER

/note= "2'-methoxyethyl residues"

modified_base 17..18

/*tag= f

/mod_base= m5c

modified_base 20

/*tag= g

/mod_base= m5c

XX WO200250244-A2.

PD 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1006 GAGCGGTGGTTACACCAT 1025
Db 20 GAGCGGTGGTTACACCAT 1
RESULT 90
AAD40895/c
ID AAD40895 standard; DNA; 20 BP.
AC AAD40895;
XX
XX 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123676.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6
FT /tag= d
FT /mod_base= m5c
FT modified_base 9
FT /tag= e
FT /mod_base= m5c
FT modified_base 11..12
FT /tag= f
FT /mod_base= m5c
FT modified_base 14
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20

FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= h
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
XX 27-JUN-2002.
PD
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 288 AATGCTGAGGAGATGACCAA 307
Db 20 AATGCTGAGGAGATGACCAA 1
RESULT 91
AAD40901/c
ID AAD40901 standard; DNA; 20 BP.
XX
AC AAD40901;
XX
XX 30-OCT-2002 (first entry)
DT
XX
DE Human HDAl antisense oligonucleotide ISIS #123682.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH

modified_base 1. .20
/tag= a
/mod_base= OTHER
modified_base 1. .5
/tag= b
/mod_base= OTHER
modified_base 1
/note= "2'-methoxyethyl residues"
modified_base 7. .8
/tag= d
/mod_base= m5c
modified_base 11
/tag= e
/mod_base= m5c
modified_base 14
/tag= f
/mod_base= m5c
modified_base 16. .20
/tag= g
/mod_base= m5c
modified_base 17
/tag= c
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modified_base 17
/note= "2'-methoxyethyl residues"
/tag= h
/mod_base= m5c

WO200250244-A2.

27-JUN-2002.

07-DEC-2001; 2001WO-US046518.

19-DEC-2000; 2000US-00745167.

(ISIS-) ISIS PHARM INC.

Monia BP, Wyatt JR;

WPI; 2002-519880/55.

Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.

Claim 3; Page 93; 120pp; English.

The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDA1). Sequences of the invention are useful for inhibiting the expression of HDA1 in cells or tissues and for treating an animal having a disease or condition associated with HDA1 e.g., hyperproliferative condition, which is cancer of hematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targeted to human HDA1 DNA

Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

485 TAAGCAGCAGCGACATCG 504

|||||

Db 20 TAAGCAGCAGCGACATCG 1
RESULT 92
AAD40903/c
ID AAD40903 standard; DNA; 20 BP.
XX
AC AAD40903;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDA1 antisense oligonucleotide ISIS #123684.
XX
KW Human; histone deacetylase 1; HDA1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1. .5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 2. .3
FT /tag= d
FT /mod_base= m5c
FT modified_base 11. .12
FT /tag= e
FT /mod_base= m5c
FT modified_base 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= f
FT /mod_base= m5c
XX
WO200250244-A2.
PN
XX
27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDA1). Sequences of the invention are useful for inhibiting the expression of HDA1 in cells or tissues and for treating an animal having a disease or condition associated with HDA1 e.g., hyperproliferative condition, which is cancer of hematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAL DNA
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred.No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 576 ATCGTCTTGGCCATCCTGGA 595
 DB 20 ATCGTCTTGGCCATCCTGGA 1
 RESULT 93
 AAD40918/c
 ID AAD40918 standard; DNA; 20 BP.
 XX
 AC AAD40918;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAL antisense oligonucleotide ISIS #123699.
 XX
 KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 5..16
 FT /tag= d
 FT /mod_base= m5c
 FT /tag= e
 FT /mod_base= m5c
 FT /tag= f
 FT /mod_base= m5c
 FT /tag= c
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 FT /note= "2'-methoxyethyl residues"
 XX
 PN WO200250244-A2.
 XX
 PD 27-JUN-2002.
 XX
 XX
 PF 07-DEC-2001; 2001WO-US046518.
 XX
 PR 19-DEC-2000; 2000US-00745167.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Wyatt JR;
 XX
 DR WPI; 2002-519880/55.
 XX
 PT Antisense compounds targeted against polynucleotides encoding Histone

PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 PT infection.
 XX
 PS Claim 3; Page 94; 120pp; English.
 XX
 CC The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAL in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAL e.g., hyperproliferative condition, which
 CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAL DNA
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred.No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 905 CCTATCTGGGATCGGTTAG 924
 DB 20 CCTATCTGGGATCGGTTAG 1
 RESULT 94
 AAD40920/c
 ID AAD40920 standard; DNA; 20 BP.
 XX
 AC AAD40920;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAL antisense oligonucleotide ISIS #123701.
 XX
 KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 1
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 3
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 8
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 13..14
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c

FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 ATCAAAGGACACGCCAAGTG 961
Db 20 ATCAAAGGACACGCCAAGTG 1

RESULT 95
AAD40934/c
ID AAD40934 standard; DNA; 20 BP.
XX
AC AAD40934;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123715.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"

FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
FT modified_base 3
FT /tag= d
FT /mod_base= m5c
FT
FT modified_base 7
FT /tag= e
FT /mod_base= m5c
FT
FT modified_base 10
FT /tag= f
FT /mod_base= m5c
FT
FT modified_base 12..13
FT /tag= g
FT /mod_base= m5c
FT
FT modified_base 15..16
FT /tag= h
FT /mod_base= m5c
FT
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
XX WO200250244-A2.
PN
XX 27-JUN-2002.
PD
XX
XX 07-DEC-2001; 2001WO-US046518.
PF
XX 19-DEC-2000; 2000US-00745167.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 96

ABV73074/c	
ID	ABV73074 standard; DNA; 20 BP.
XX	
AC	ABV73074;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	Human HDAC-1 mRNA inhibiting antisense oligo HDAC1 AS2.
XX	
KW	Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
KW	HDAC-1; human; cancer; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO200269947-A2.
XX	
PD	12-SEP-2002.
XX	
PF	14-JAN-2002; 2002WO-IB002002.
XX	
PR	12-JAN-2001; 2001US-0261522P.
PR	12-JAN-2001; 2001US-0261674P.
XX	
PA	(METH-) METHYLGENE INC.
XX	
PI	Besterman JM, Bonfils C, Woo SH, Vaisburg A, Delorme D;
PI	Fournel M, Lavoie R, Li Z;
XX	
DR	WPI; 2002-750436/81.
XX	
PT	Inhibition of HDAC-4 activity in a cell useful for treating e.g. cancer
PT	involves contacting the cell with an antisense oligonucleotide or a small
PT	molecule inhibitor of HDAC-4.
XX	
PS	Disclosure; Page 32; 124pp; English.
XX	
CC	The invention relates to inhibition of histone deacetylase (HDAC)-4
CC	activity in a cell that involves contacting the cell with an antisense
CC	oligonucleotide complementary to a region of RNA encoding a portion of
CC	HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for
CC	inhibiting neoplastic cell proliferation in an animal (preferably human)
CC	and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
CC	specific antisense and mismatch oligonucleotides
XX	
SQ	Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;	
Best Local Similarity 100.0%; Pred. No. 26;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1565 CCTCTCCAGCTCTGGCTTCC 1584
Db	20 CCTCTCCAGCTCTGGCTTCC 1
RESULT 97	
ABV73073/c	
ID	ABV73073 standard; DNA; 20 BP.
XX	
AC	ABV73073;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	Human HDAC-1 mRNA inhibiting antisense oligo HDAC1 AS1.
XX	
KW	Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
KW	HDAC-1; human; cancer; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO200269947-A2.
Query Match 1.2%; Score 20; DB 1; Length 20;	
Best Local Similarity 100.0%; Pred. No. 26;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1585 TGCTGAGTCCCTCAGTTTC 1604
Db	20 TGCTGAGTCCCTCAGTTTC 1
RESULT 98	
ABK87723/c	
ID	ABK87723 standard; DNA; 20 BP.
XX	
AC	ABK87723;
XX	
DT	07-OCT-2002 (first entry)
XX	
DE	Human histone deacetylase isoform 1 antisense oligonucleotide AS1.
XX	
KW	Human; ss; histone deacetylase; HDAC-1; cancer; cytostatic; antisense;
KW	tumour suppressor; cell proliferation; tumour; programmed cell death;
KW	necrotic cell death.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	modified_base 1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone"
FT	modified_base 1..4
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "These nucleotides have 2'-O-methyl groups
FT	attached to their sugar residues"
FT	modified_base 17..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "These nucleotides have 2'-O-methyl groups
FT	attached to their sugar residues"
XX	
PN	US2002061860-A1.

XX 23-MAY-2002.
XX
XX
PF 06-AUG-2001; 2001US-00817913.
XX
XX
PR 24-MAR-2000; 2000US-0192157P.
XX
XX
PA (LIZZ/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J.
XX
PI Li Z, Bonfils C, Besterman J;
XX
XX WPI; 2002-507650/54.
XX
XX Agent that specifically inhibits an isoform of histone deacetylase,
PT useful for treating cancer and other cell proliferative diseases,
PT preferably comprises an antisense oligonucleotide.
XX
XX Claim 24; Page 6; 60pp; English.
XX
XX The invention relates to an agent that inhibits an isoform of histone
CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense
CC oligonucleotide. Also included are inhibiting an HDAC isoform in a cell
CC by treatment with the agent, identifying an HDAC isoform that is required
CC for induction of cell proliferation or differentiation and inhibiting
CC cell proliferation by treatment with two antisense oligonucleotides or
CC small molecules that inhibit a specific HDAC isoform, or antisense
CC oligonucleotide or small molecules that inhibit DNA methyltransferase.
CC The agent therefore acts as a tumour suppressor. The agents are used to
CC treat diseases of cell proliferation and differentiation (e.g. cancer and
CC tumours), by inducing growth retardation, growth arrest or
CC programmed/necrotic cell death, specifically neoplastic cell
CC proliferation in humans. The agents are selective for particular
CC isoforms, compared to known inhibitors which are not selective. The
CC present sequence is an antisense oligonucleotide of the invention
CC targeting the polynucleotide which encodes the HDAC-1 isoform
XX
XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1585 TGCTGAGTCCCTCACGTTTC 1604
Db 20 TGCTGAGTCCCTCACGTTTC 1
RESULT 99
ABK87724/c
ID ABK87724 standard; DNA; 20 BP.
XX
AC ABK87724;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human histone deacetylase isoform 1 antisense oligonucleotide AS2.
XX
KW Human; ss; histone deacetylase; HDAC-1; cancer; cytostatic; antisense;
KW tumour suppressor; cell proliferation; tumour; programmed cell death;
KW necrotic cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= b
FT /mod_base= OTHER

FT /note= "These nucleotides have 2'-O-methyl groups
attached to their sugar residues"
modified_base 17..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "These nucleotides have 2'-O-methyl groups
attached to their sugar residues"
XX
PN US2002061860-A1.
XX
PD 23-MAY-2002.
XX
PF 06-AUG-2001; 2001US-00817913.
XX
PR 24-MAR-2000; 2000US-0192157P.
XX
XX (LIZZ/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J.
XX
PI Li Z, Bonfils C, Besterman J;
XX
XX WPI; 2002-507650/54.
XX
XX Agent that specifically inhibits an isoform of histone deacetylase,
PT useful for treating cancer and other cell proliferative diseases,
PT preferably comprises an antisense oligonucleotide.
XX
XX Claim 24; Page 6; 60pp; English.
XX
XX The invention relates to an agent that inhibits an isoform of histone
CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense
CC oligonucleotide. Also included are inhibiting an HDAC isoform in a cell
CC by treatment with the agent, identifying an HDAC isoform that is required
CC for induction of cell proliferation or differentiation and inhibiting
CC cell proliferation by treatment with two antisense oligonucleotides or
CC small molecules that inhibit a specific HDAC isoform, or antisense
CC oligonucleotide or small molecules that inhibit DNA methyltransferase.
CC The agent therefore acts as a tumour suppressor. The agents are used to
CC treat diseases of cell proliferation and differentiation (e.g. cancer and
CC tumours), by inducing growth retardation, growth arrest or
CC programmed/necrotic cell death, specifically neoplastic cell
CC proliferation in humans. The agents are selective for particular
CC isoforms, compared to known inhibitors which are not selective. The
CC present sequence is an antisense oligonucleotide of the invention
CC targeting the polynucleotide which encodes the HDAC-1 isoform
XX
XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTCGGCTTC 1584
Db 20 CCTCTCCAGCTCTCGGCTTC 1
RESULT 100
ABZ76476/c
ID ABZ76476 standard; DNA; 20 BP.
XX
AC ABZ76476;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human HDAC1 mRNA targeting antisense oligo HDAC1 AS1.
XX
KW HDAC; histone deacetylase; cytostatic; vasotropic; antiproliferative;
KW antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.

XX WO2003024448-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029017.
 XX
 XX 14-SEP-2001; 2001US-0322402P.
 XX
 XX 26-JUN-2002; 2002US-0391728P.
 XX
 XX (METH-) METHYLGENE INC.
 XX
 XX Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppe S;
 XX Frechette S, Bouchain G;
 XX
 XX WPI; 2003-342612/32.
 XX
 XX New histone deacetylase inhibitors, useful for treatment of proliferative
 XX diseases or conditions e.g. cancer.
 XX
 XX Disclosure; Page 72; 347pp; English.
 XX
 XX The invention relates to histone deacetylase inhibitors of specified
 XX formulae and their salts. The compounds inhibit histone deacetylase
 XX (HDAC) enzymatic activity. They can be used for treating cell
 XX proliferative diseases or condition (e.g. cancer, restenosis and
 XX psoriasis). Sequences ABZ76476-492 represent antisense and mismatch
 XX oligonucleotides targeting the 5'- UTR (untranslated region) and 3'-UTRS
 XX of the human HDAC1-8 genes
 XX
 XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 1.2%; Score 20; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 26;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1585 TGCTGAGTCCCTCAGTTTC 1604
 DB 20 TGCTGAGTCCCTCAGTTTC 1
 |||||
 RESULT 101
 ABZ76477/C
 ID ABZ76477 standard; DNA; 20 BP.
 XX
 XX AC ABZ76477;
 XX
 XX 23-JUN-2003 (first entry)
 XX
 XX Human HDAC1 mRNA targeting antisense oligo HDAC1 AS2.
 XX
 XX HDAC; histone deacetylase; cytostatic; vasotropic; antipsoriatic;
 XX antisense; ss.
 XX
 XX Synthetic.
 XX OS Homo sapiens.
 XX
 XX WO2003024448-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029017.
 XX
 XX 14-SEP-2001; 2001US-0322402P.
 XX
 XX 26-JUN-2002; 2002US-0391728P.
 XX
 XX (METH-) METHYLGENE INC.
 XX
 XX Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppe S;
 XX Frechette S, Bouchain G;
 XX
 XX WPI; 2003-342612/32.
 XX

PT deacetylase isoforms, is useful in modulating cell proliferation
PT especially neoplasia.
XX
PS Claim 7; SEQ ID NO 17; 52pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising a
CC nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
CC specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
CC oligonucleotide is complementary to a region of RNA or double stranded
CC DNA. The oligonucleotide is useful in inhibiting one or more histone
CC deacetylases isoforms in a cell comprising contacting the cell with the
CC oligonucleotide. Cell proliferation is inhibited in the contacted cell
CC which undergoes growth retardation and growth arrest. The contacted cell
CC undergoes programmed and necrotic cell death. The oligonucleotide is also
CC useful in inhibiting neoplastic cell proliferation in an animal,
CC preferably a human. The oligonucleotide is also useful in identifying a
CC histone deacetylase isoform that is required for the induction of cell
CC proliferation comprising contacting the histone deacetylase isoform with
CC the oligonucleotide where a decrease in induction of cell proliferation
CC indicates that the isoform is required for the induction of cell
CC proliferation. The above method is also applicable to identifying
CC isoforms required for cell proliferation. The oligonucleotide is useful
CC in identifying an isoform required for the induction of cell
CC differentiation, where an induction of cell differentiation indicates
CC that the isoform is required for differentiation. Also useful in
CC modulating cell proliferation especially neoplasia. The present sequence
CC an antisense oligonucleotide directed against an HDAC isoform containing
CC mismatched bases.
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 103
ADC21704/C
ID ADC21704 standard; DNA; 20 BP.
XX
AC ADC21704;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human HDAC-1 antisense oligonucleotide AS2.
XX
KW Human; histone deacetylase; isoform; HDAC-1; HDAC-2; HDAC-3; HDAC-4;
KW HDAC-5; HDAC-6; HDAC-7; HDAC-8; antisense gene therapy;
KW cell proliferation; programmed cell death; necrotic cell death;
KW neoplastic cell proliferation; cell differentiation; neoplasm; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methyl residues"
FT modified_base 17..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methyl residues"
XX
PN US2002137162-A1.
XX

PD 26-SEP-2002.
XX
PF 26-MAR-2001; 2001US-00817538.
XX
PR 24-MAR-2000; 2000US-0192157P.
PR 12-JAN-2001; 2001US-0261522P.
XX (LIZZ/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J M.
XX
PI Li Z, Bonfils C, Besterman JM;
XX WPI; 2003-786641/74.
DR
XX New antisense oligonucleotide that inhibits one or more specific histone
PT deacetylase isoforms, is useful in modulating cell proliferation.
PT especially neoplasia.
XX
PS Claim 7; SEQ ID NO 18; 52pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising a
CC nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
CC specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
CC oligonucleotide is complementary to a region of RNA or double stranded
CC DNA. The oligonucleotide is useful in inhibiting one or more histone
CC deacetylases isoforms in a cell comprising contacting the cell with the
CC oligonucleotide. Cell proliferation is inhibited in the contacted cell
CC which undergoes growth retardation and growth arrest. The contacted cell
CC undergoes programmed and necrotic cell death. The oligonucleotide is also
CC useful in inhibiting neoplastic cell proliferation in an animal,
CC preferably a human. The oligonucleotide is also useful in identifying a
CC histone deacetylase isoform that is required for the induction of cell
CC proliferation comprising contacting the histone deacetylase isoform with
CC the oligonucleotide where a decrease in induction of cell proliferation
CC indicates that the isoform is required for the induction of cell
CC proliferation. The above method is also applicable to identifying
CC isoforms required for cell proliferation. The oligonucleotide is useful
CC in identifying an isoform required for the induction of cell
CC differentiation, where an induction of cell differentiation indicates
CC that the isoform is required for differentiation. Also useful in
CC modulating cell proliferation especially neoplasia. The present sequence
CC an antisense oligonucleotide directed against an HDAC isoform containing
CC mismatched bases.
XX
SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCAGCTCTGGCTTCC 1584
|||||
Db 20 CCTCTCAGCTCTGGCTTCC 1

RESULT 104
AAS06923/C
ID AAS06923 standard; DNA; 24 BP.
XX
AC AAS06923;
XX
DT 11-SEP-2003 (revised)
DT 12-SEP-2001 (first entry)
XX
DE HPIV1 HN gene PCR primer.
XX
KW Infectious chimeric parainfluenza virus; antigenic determinant;
KW nucleocapsid phosphoprotein; large polymerase; attenuated vaccine;
KW human PIV1; HPIV1; HPIV2; HPIV3; RSV; pathogen; measles; PCR primer;
KW respiratory syncytial virus; respiratory tract infection; ss.
XX
OS Human parainfluenza virus 1.


```

Query Match      1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      633 ATTGATATTCAACCATGCTGACGGC 656
      ||||| ||||| ||||| ||||| |||||
Db      24  ATTGCTATTCAACCATGACAGCGC 1

```

RESULT 105
AAA55797/C
ID AAA55797 standard; DNA; 20 BP.
XX
AC AAA55797;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:40.
XX
KW Human; DNA methyltransferase; DNA MeTase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX

```

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGAGCGCTCTGTCACTC 81
      |||||
DB      20 CCTGAGCGCTCTGTCACTC 1

```

RESULT 106
AAA55799/C
ID AAA55799 standard; DNA; 20 BP.
XX
XX AC AAA55799;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:42.
XX
KW Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
KW

XX Homo sapiens.
OS
XX
XX WO200023112-A1.
PN
XX
XX 27-APR-2000.
PD
XX
XX 19-OCT-1999; 99WO-US024278.
PF
XX
XX 19-OCT-1998; 98US-0104804P.
PR
XX
XX (METH-) METHYLGENE INC.
PA
XX
XX Besterman JM, Macleod AR, Siders WM;
PI
XX
XX WPI; 2000-339532/29.
DR
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
PT
XX
PS Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1531 GGGTCAAGGAGGAGGCCAAG 1550
Db 20 GGGTCAAGGAGGAGGTCAAG 1
RESULT 107
AAH43107/c
ID AAH43107 standard; DNA; 20 BP.
XX
AC AAH43107;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 62-81.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX

OS Synthetic.
XX
XX WO200138322-A1.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-IB001881.
PF
XX
XX 23-NOV-1999; 99US-0167035P.
PR
XX
XX (METH-) METHYLGENE INC.
PA
XX
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
PI
XX
XX WPI; 2001-432601/46.
DR
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
PT
XX
XX Disclosure; Page 40; 147pp; English.
PS
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 62 CCTGAGCGGCTCTGTCACTC 81
Db 20 CCTGAGCGGCTCTGTCACTC 1
RESULT 108
AAH43109/c
ID AAH43109 standard; DNA; 20 BP.
XX
AC AAH43109;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 1531-1550.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
XX WO200138322-A1.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-IB001881.
PF
XX
XX 23-NOV-1999; 99US-0167035P.
PR
XX
XX (METH-) METHYLGENE INC.
PA
XX
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
PI
XX
XX WPI; 2001-432601/46.
DR
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-

PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAAGGAGGAGGCCAAG 1550
Db 20 GGGTCAAGGAGGAGGTCAAG 1

RESULT 109
AAD40902/c
ID AAD40902 standard; DNA; 20 BP.
XX AAD40902;
AC
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAC1 antisense oligonucleotide ISIS #123683.
XX
KW Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /tag= d
FT /mod_base= m5c
FT modified_base 3
FT /tag= e
FT /mod_base= m5c
FT modified_base 6
FT /tag= f
FT /mod_base= m5c
FT modified_base 12..13
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16
FT /tag= h
FT /mod_base= m5c
FT modified_base 19
FT /tag= i
FT /mod_base= m5c

XX WO200250244-A2.
PN
XX
PD 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAC1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAC1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAC1 e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAC1 DNA
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 490 AGCAGACGGACATCGCCGTG 509
Db 20 AGCAGACGGACATCGCTGTG 1

RESULT 110
AAD40927/c
ID AAD40927 standard; DNA; 20 BP.
XX
AC AAD40927;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAC1 antisense oligonucleotide ISIS #123708.
XX
KW Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b

FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT 7 /tag= d
FT /mod_base= m5c
FT 9
FT /tag= e
FT /mod_base= m5c
FT 10
FT /tag= f
FT /mod_base= m5c
FT 13
FT /tag= g
FT /mod_base= m5c
FT 15.20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX

PN WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.

PS Claim 3; Page 94; 120pp; English.

XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAC1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAC1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAC1 e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAC1 DNA

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1246 TCACAGCGCAGCGGATTCCT 1265
||||| |||||||
Db 20 TCACAAATGCAGCGGATTCCT 1

RESULT 111

ABT39526/c

ID ABT39526 standard; DNA; 17 BP.

XX AC ABT39526;

XX

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 5163.

DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PS Disclosure; Page 637; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 CTCCTATCTGGGATC 918
||||| |||||||
Db 17 CTCCTATCTGGGATC 1

RESULT 112

ABT39292

ID ABT39292 standard; DNA; 17 BP.

XX AC ABT39292;

XX 12-JUN-2003 (first entry)

XX

PF 22-DEC-2000; 2000EP-00403659.
XX
PR 22-DEC-2000; 2000EP-00403659.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bernard M, Sourdille P, Guyomarch H;
XX
DR WPI; 2002-550410/59.
XX
PT Map of wheat D genome comprising the genome location of a microsatellite
PT marker, useful for e.g. identifying genes responsible for a desired
PT phenotypic trait, especially quantitative trait loci in wheat, and
PT diseases.
XX

Claim 4; Page 10; 105pp; English.

The invention relates to a map of the bread wheat D genome comprising the genome location of a microsatellite marker selected from a group of 185 such markers (ABQ92733-ABQ92917). The invention also encompasses the use of left (ABQ92918-ABQ93102) and right (ABQ93103-ABQ93287) primers to amplify and detect the microsatellite markers, and to identify genes responsible for a phenotypic trait of interest in wheat. Wheat is an allohexaploid species consisting of 3 diploid genomes designated A, B and D, resulting from two successive intercrossings involving at least three different species. The D genome is thought to have been introduced in the most recent intercrossing, between the amphiploid AABB and Triticum tauschii (DD), probably involving only a limited number of genotypes of both species. Due to its polyploid genome, the large size of its genome, and its low level of polymorphism, the genetic mapping of wheat has to date been difficult. Microsatellites are tandemly repeated sequences between one and six nucleotides long, and are very polymorphic in length, mainly due to polymerase slippage during replication. This high degree of polymorphism makes them especially suitable for the genetic mapping of species which show little intraspecies polymorphism, such as wheat. In addition, microsatellites are codominant, and exhibit Mendelian inheritance. The 185 microsatellite markers of the invention are developed from the ancestral diploid donor species Triticum tauschii and map to the wheat D genome, which is less polymorphic than the A or B genomes. These microsatellite markers thus help to overcome some of the problems associated with the genetic mapping of wheat. The wheat D genome map and the microsatellite markers and associated primers of the invention are useful for identifying genes responsible for a phenotypic trait of interest, most notably QTLs (quantitative trait loci). In particular they may be used for analysing genes and alleles implicated in disease and for identifying development factors, quality factors and factors conferring resistance to pathogens and xenobiotics. The microsatellite markers, and associated primers may be also be used in mapping and genotyping diploid and polyploid species of Triticum, particularly Aegilops, Triticum monococcum, Triticum durum, Triticum aestivum, or related species; for identifying cultivars and hybrids of Triticum and related species; to assess whether or not a product comprises wheat or a related species; and to assess whether or not a product comprises genetically modified wheat. The present sequence represents a specifically claimed Triticum tauschii/wheat genome D microsatellite marker left PCR primer of the invention. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 20 BP; 10 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1187 GGAGAAGATCAACACGGAC 1206
|||||
Db 1 GGAGAAAGCAACACGGAC 20

RESULT 115
ABZ92578/c
ID ABZ92578 standard; DNA; 20 BP.
XX

AC ABZ92578;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7820; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAGATCAA 1198
|||||
Db 20 GAGGACCTGGAGAGATCAA 1

RESULT 116
ACC86770/c
ID ACC86770 standard; DNA; 20 BP.
XX

XX DE Mouse HUI77/HUIV26 antibody related PCR primer SeqID198.
XX KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; HUI77; HUIV26; mouse; murine; PCR; primer; ss;
XX heavy chain.
XX OS Mus musculus.
XX PN WO2003046204-A2.
XX PD 05-JUN-2003.
XX PF 26-NOV-2002; 2002WO-US038147.
XX PR 26-NOV-2001; 2001US-00995529.
XX PR 06-DEC-2001; 2001US-00011250.
XX PA (CELL-) CELL MATRIX INC.
XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX WPI; 2003-513649/48.
XX PF New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX Example 1; SEQ ID NO 198; 232pp; English.
XX CC This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is that of a mutagenic PCR primer for amplification of
CC the sequence encoding the heavy chain of mouse HUI77 or HUIV26 antibodies
CC and used in the exemplification of the invention.
XX SQ Sequence 17 BP; 0 A; 3 C; 2 G; 11 T; 0 U; 1 Other;

Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 53;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 119
AAT27507/C
ID AAT27507 standard; DNA; 20 BP.
XX AAT27507;
AC
XX 04-JUL-1996 (first entry)
DT
XX Human c-raf kinase 3' untranslated region antisense oligonucleotide.
DE
XX Antisense; anti-proliferative; tumour; cancer; raf; oncogene;
KW phosphorothioate; 2' sugar modification; psoriasis; restenosis; ss.
XX Synthetic.
OS

FH Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "opt. phosphorothioate linked"
FT misc_feature 10..20
FT /*tag= b
FT /note= "contain 2'-O-methyl modifications"
XX
PN WO9532987-A1.
XX
PD 07-DEC-1995.
XX
XX 31-MAY-1995; 95WO-US007111.
PF
XX 31-MAY-1994; 94US-00250856.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Boggs RT;
PI
XX WPI; 1996-030518/03.
DR
XX Oligo:nucleotide(s) targetted to nucleic acids encoding human raf -
PT capable of inhibiting raf expression, used in treatment of
PT hyperproliferative disorders.
XX Claim 10; Page 18; 65pp; English.
XX AAT27481-T27507 are human c-raf kinase antisense oligonucleotides used
CC for the inhibition of raf expression. The oligonucleotides (ONS) are
CC targeted to either coding region, start or stop signal or 5' or 3',
CC untranslated region (UTR) mRNA encoding human c-raf. The ONS may be
CC phosphorothioate linked and may contain modifications at the 2' position
CC of the sugar moiety. ONS are pref. complementary to either 3' or 5' UTRs,
CC phosphorothioate linked and contain 2'-O-alkyl sugar modifications. The
CC ONS are used to inhibit expression of human raf in partic. in conditions
CC associated with hyperproliferation e.g. cancer, restenosis, and psoriasis
XX SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGCAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 120
AAX36464/C
ID AAX36464 standard; DNA; 20 BP.
XX
AC AAX36464;
XX
DT 06-JUL-1999 (first entry)
XX
DE Chimeric 2'-O-methyl oligo for c-raf inhibition.
XX
KW RNaseH; RNA cleavage; DNA cleavage; hybridisation; protein kinase C gene;
KW gene expression modulation; ras; raf; therapy; AIDS; atherosclerosis;
KW infection; cell growth; ss.
XX
OS Synthetic.
XX
PN WO9730067-A1.
XX
PD 21-AUG-1997.
XX
PF 07-FEB-1997; 97WO-US002043.
XX
PR 14-FEB-1996; 96US-0011620P.
XX

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01-AUG-1995;    95GB-00015743.
19-SEP-1995;    95GB-00019130.
(CIBA ) CIBA GEIGY AG.
Love WG, Phillips JA, Nicklin PL, Hamilton KO;
WPI; 1997-145363/13.
Inhibiting human raf expression, partic. for treating cancer - using an oligonucleotide targetted to mRNA encoding human raf entrappeded in sterically stabilised liposome(s).
Claim 16; Page 19; 27pp; English.
AAT59716-28 are preferred oligonucleotides which are targeted to mRNA encoding human raf and are capable of inhibiting raf expression. Compositions containing the oligonucleotides entrappeded in sterically stabilised liposomes are claimed. The compsns. can be used for inhibiting the expression of human raf. They can be used for the treatment of mammalian cancer, partic. human cancer e.g. lung, stomach, renal, breast, laryngeal, pancreatic, colorectal cancer and malignant melanoma. In particular the compsns. can inhibit abnormal raf expression and retain anti-hyperproliferative activity after prolonged circulation in the bloodstream. They facilitate the reduction of accumulation of ONs in non-target organs and a reduction of acute and chronic side effects during prolonged treatment. ON18, 19 and 21 are chimeric oligonucleotides with uniform phosphorothioate backbones, and substituted with methoxy at the 2' position of the sugar moiety as indicated above. ON21 is targeted to the 3'UTR of c-raf
Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match          1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1507 AGGAGGAGAAGCCAGAAG 1524
Db       19 AGGAGGAGAAGCCAGCAG 2
|||||||
RESULT 122
AAT62157/C
ID      AAT62157 standard; DNA; 20 BP.
AC      AAT62157;
XX
DT      01-DEC-1997 (first entry)
XX
DE      Human c-raf and dextran sulphate mRNA targetting oligonucleotide ON21.
XX
KW      Cancer; anionic polysaccharide; human; lung cancer; stomach cancer; renal cancer; breast cancer; laryngeal cancer; pancreatic cancer; colorectal cancer; malignant melanoma; tumour; ss.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      misc_feature 1..20
FT      /*tag= a
FT      /note= "Phosphorothioate backbone; optionally being substituted at the 2'-position of the sugar moiety by a methoxy group at positions 10 to 20"
XX
PN      WO9710829-A1.
XX
PD      27-MAR-1997.
XX
PF      12-SEP-1996; 96WO-GB002245.
XX
PR      19-SEP-1995; 95GB-00019109.
XX

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PA (CIBA) CIBA GEIGY AG.
XX
PI Nicklin PL, Steward A;
XX
DR WPI; 1997-202610/18.
XX
XX
PT Composition for cancer treatment - comprising anionic polysaccharide, and
PT oligo:nucleotide targetted to mRNA encoding human c-raf and dextran
PT sulphate.
XX
XX
PS Claim 16; Page 15; 21pp; English.
XX
XX
CC A pharmaceutical composition has been developed comprising an
CC oligonucleotide, targeted to human raf encoding mRNA, and an anionic
CC polysaccharide. The present sequence represents a specifically claimed
CC oligonucleotide for use in the composition. The composition can be used
CC to treat mammalian cancer, especially human lung, stomach, renal, breast,
CC laryngeal, pancreatic or colorectal cancer, or malignant melanoma. The
CC anionic polysaccharide increases tumour uptake of the oligonucleotide,
CC particularly an oligonucleotide targeted to human raf encoding mRNA
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 123
AAZ15070/c
ID AAZ15070 standard; DNA; 20 BP.
XX
AC AAZ15070;
XX
DT 20-MAR-2003 (revised)
DT 16-APR-1999 (first entry)
XX
XX
DE c-raf antisense chimeric oligonucleotide of the invention.
XX
KW Nuclease resistant; ribofuranosyl moiety; 2'-aminoalkoxy; tumour;
KW 2'-imidazolylalkoxy; modulation; activity; AIDS; atherosclerosis;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "phosphorothioated"
XX
PN US5872232-A.
XX
PD 16-FEB-1999.
XX
PF 06-JUN-1995; 95US-00471973.
XX
PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 12-AUG-1991; 91WO-US005720.
PR 05-MAR-1992; 92US-00835932.
PR 01-JUL-1992; 92US-00854634.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Kawasaki AM;
XX
DR WPI; 1999-166721/14.
XX
PT New 2'-O-modified oligo-nucleotide(s) - comprising nucleotide(s)

PT comprising a 2'-aminoalkoxy or 2'-imidazolylalkoxy substituent, used for
PT hybridisation to RNA or DNA.
XX
XX
PS Example 31; Col 50; 48pp; English.
XX
XX
CC The present oligonucleotide exemplifies the oligonucleotides of the
CC invention. Oligonucleotides of the invention are nuclease resistant, and
CC comprise covalently-bound nucleosides that individually include a ribose
CC or deoxyribose sugar portion and base portion where the nucleosides are
CC joined together by internucleoside linkages such that the base portion of
CC the nucleosides form a mixed base sequence that is complementary to a RNA
CC base sequence or to a DNA base sequence. At least one of the nucleosides
CC has a modified ribofuranosyl moiety bearing a 2'-aminoalkoxy or 2'-
CC imidazolylalkoxy substituent. The nuclease resistant compounds can be
CC used for modulating the activity of DNA or RNA. They can be used for
CC treating organisms having a disease characterised by the undesired
CC production of a protein. Diverse organisms such as bacteria, yeast,
CC protozoa, algae, plant and higher animal forms including warm-blooded
CC animals can be treated in this manner. The compounds can be used for
CC treating e.g. AIDS, atherosclerosis or tumours. They can also be used in
CC diagnostic methods for detecting the presence or absence of abnormal RNA
CC molecules, or abnormal or inappropriate expression of normal RNA
CC molecules in organisms or cells. (Updated on 20-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 124
AAZ11537/c
ID AAZ11537 standard; DNA; 20 BP.
XX
AC AAZ11537;
XX
DT 05-NOV-1999 (first entry)
XX
DE Human c-raf kinase antisense oligo ISIS # 7853.
XX
KW Human; raf; diagnosis; abnormal proliferative state; hyperproliferation;
KW cancer; psoriasis; blood vessel restenosis; c-raf kinase; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5952229-A.
XX
PD 14-SEP-1999.
XX
PF 26-NOV-1996; 96US-00756806.
XX
PR 31-MAY-1994; 94US-00250856.
PR 31-MAY-1995; 95WO-US007111.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Boggs RT, Monia BP;
XX
DR WPI; 1999-527018/44.
XX
PT Oligonucleotides targeted to human raf mRNA useful for treating and
PT diagnosing abnormal proliferative states and inhibiting raf expression.
XX
PS Claim 1; Col 11; 29pp; English.
XX
CC The invention provides antisense oligonucleotides targeted to mRNA

CC encoding human raf and capable of inhibiting raf expression. The
CC antisense oligonucleotides are useful for treating and diagnosing
CC abnormal proliferative states and hyperproliferation (e.g. cancer,
CC psoriasis, or blood vessel restenosis), and inhibiting raf expression.
CC Sequences AAZ11511-537 and AAZ11565-573 represent antisense
CC oligonucleotides for human c-raf kinase
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
DB 19 AGGAGGAGAGCCAGCAG 2
RESULT 125
AAX05468/c
ID AAX05468 standard; DNA; 20 BP.
XX
AC AAX05468;
XX
DT 20-APR-1999 (first entry)
XX
DE Chimeric antisense oligo for c-raf gene.
XX
KW Nuclease resistant; modified; deoxyfuranosyl moiety; therapy; infection;
KW AIDS; atherosclerosis; tumour; c-raf; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "contains phosphorothioate linkages; optional 2' O
FT -methyl modification on some base pairs"
XX
PN US5859221-A.
XX
PD 12-JAN-1999.
XX
PF 06-JUN-1995; 95US-00468037.
XX
PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 12-AUG-1991; 91WO-US005720.
PR 05-MAR-1992; 92US-00835932.
PR 01-JUL-1992; 92US-00854634.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Kawasaki AM;
XX
XX WPI; 1999-120005/10.
DR
XX Nuclease resistant oligonucleotide analogues - having nucleosides
PT including modified deoxyfuranosyl moiety bearing 2'-substituent to
PT increase binding affinity.
XX
PS Example 31; Col 51; 49pp; English.
XX
CC The invention relates to a nuclease resistant compound that hybridises
CC with RNA or DNA. The compound comprises covalently-bound nucleosides that
CC individually include a ribose or deoxyribose sugar portion and a base
CC portion, where the nucleosides are joined together by internucleoside
CC linkages such that the base portion of the nucleosides form a mixed base
CC sequence that is complementary to a RNA base sequence or to a DNA base
CC sequence; and where at least 1 of the nucleosides includes a modified
CC deoxyfuranosyl moiety bearing a 2'-substituent selected from cyano,
CC fluoromethyl, thioalkoxyl, alkylsulphinyl, alkylsulphonyl, allyloxy and

CC alkeneoxy groups. The nuclease resistant oligonucleotides (ONs) can bind
CC to and modulate the activity of DNA or RNA and can be used for treating
CC organisms having a disease characterised by the undesired production of a
CC protein. They can be used in therapeutic or prophylactic treatment in
CC organisms such as bacteria, yeast, protozoa, algae, plant and higher
CC animal forms including warm-blooded animals. The ONs can also be used for
CC treating infections, AIDS, atherosclerosis or tumours. The products can
CC be used for detection and diagnosis. The ONs provide enhanced binding to
CC targets. Increased binding of 2'-sugar modified sequence-specific ONs
CC provides superior potency and specificity compared to phosphorus-modified
CC ONs. The present sequence represents a chimeric antisense oligo for c-raf
CC gene
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
DB 19 AGGAGGAGAGCCAGCAG 2
RESULT 126
AAZ10296/c
ID AAZ10296 standard; DNA; 20 BP.
XX
AC AAZ10296;
XX
DT 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
DE Oligonucleotide used to inhibit c-raf gene expression.
XX
KW Antisense oligonucleotide; c-raf; nuclease resistance;
KW RNAse H strand cleavage; phosphorothioate; oligonucleotide therapeutic;
KW AIDS; atherosclerosis; ss.
XX
OS Synthetic.
XX
PN US5955589-A.
XX
PD 21-SEP-1999.
XX
PF 06-JUN-1995; 95US-00465880.
XX
PR 24-DEC-1991; 91US-00814961.
PR 23-DEC-1992; 92WO-US011339.
PR 21-JUN-1994; 94US-00244993.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cook PD;
XX
XX WPI; 1999-539598/45.
DR
XX Oligonucleotides eliciting RNAse H activity useful for diagnosis and
PT treatment of diseases e.g AIDS or atherosclerosis.
PT
XX Example 14; Col 24; 34pp; English.
PS
XX
CC The present sequence represents a phosphorothioate antisense
CC oligonucleotide used to inhibit c-raf gene expression. The
CC oligonucleotide is a gapped 2' modified oligonucleotide, whereby one part
CC has at least two consecutive 2'-F (2'-H) nucleotides and the second part
CC has at least five consecutive nucleotides with 2'-H sugar moieties. The
CC modified oligonucleotide has increased nuclease resistance, and increased
CC binding affinity for substrates. The oligonucleotide elicits RNAse H
CC strand cleavage of specific RNAs. Oligonucleotides of the invention are
CC useful for the diagnosis, detection and treatment of conditions
CC susceptible to oligonucleotide therapeutics (e.g. AIDS and
CC atherosclerosis). (Updated on 20-MAR-2003 to correct PR field.)
CC

XX SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 127
AAZ48166/c
ID AAZ48166 standard; DNA; 20 BP.
XX AC AAZ48166;
XX DT 14-MAR-2000 (first entry)
XX DE C-raf chimeric phosphorothioate oligonucleotide SEQ ID NO:13.
XX KW Polyribonucleotide solid phase synthesis; diagnosis; hybridisation;
KW protein production modulation; 2'-deoxyfuranosyl moiety; anti-HIV;
KW antiarteriosclerotic; nuclease resistant; atherosclerosis; AIDS;
KW abnormal cell proliferation; tumour formation; ss.
XX OS Synthetic.
OS US6005087-A.
PN US6005087-A.
XX PD 21-DEC-1999.
XX PF 05-MAR-1998; 98US-00035357.
XX PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 12-AUG-1991; 91WO-US005720.
PR 05-MAR-1992; 92US-00835932.
PR 01-JUL-1992; 92US-00854634.
PR 06-JUN-1995; 95US-00468037.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Kawasaki AM, Cook PD;
XX WPI; 2000-072074/06.
DR Nuclease resistant oligonucleotides useful as research agents, diagnostic agents, and in the treatment of atherosclerosis and AIDS.
XX Example 31; Col 51; 49pp; English.
CC The present invention describes nuclease resistant oligonucleotides (I) comprising 2'-fluoro modified ribofuranosyl nucleotides. (I) comprise covalently bound nucleotides, where the nucleotides are joined together by: (a) internucleotide linkages such that the base portion of the nucleotides forms a mixed base sequence; and (b) at least one of the nucleotides includes a modified ribofuranosyl group bearing a 2'-fluoro substituent; provided that at least two of the nucleotides are 2'-fluoro modified ribofuranosyl nucleotides when the internucleotide linkages are phosphodiester nucleotides. (I) bind to their target mRNA and inhibit its expression. (I) are resistant to nuclease degradation and hybridise with appropriate strength and fidelity to its target RNA/DNA. (I) are also useful as research agents, diagnostic agents and as oligonucleotide therapeutics. (I) may be used to treat atherosclerosis following angioplasty to prevent reocclusion of the treated arteries. (I) may also be used in conjunction with AZT to treat AIDS patients. (I) have been used to modulate the expression of RAF gene, a cellular gene whose activate form has been implicated in abnormal cell proliferation and tumour formation. (I) are also used to modulate the expression of protein kinase C. (I) exhibit hybridisation properties of higher quality than phosphorous modified oligonucleotide duplexes containing

CC methylphosphonates, phosphoramidates and phosphate triesters. The present sequence represent an oligonucleotide used in the exemplification of the present invention
XX SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 128
AAA73515/c
ID AAA73515 standard; DNA; 20 BP.
XX AC AAA73515;
XX DT 28-NOV-2000 (first entry)
XX DE c-raf kinase antisense oligonucleotide #36 (Isis #7853).
XX KW Human; c-raf; protein kinase; antisense oligonucleotide; cancer;
KW signal transduction; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation; stenosis;
KW restenosis; inflammatory disorder; tissue graft rejection;
KW endotoxin shock; glomerular nephritis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= a
FT /note= "All or some nucleotides are optionally with 2'-methoxyethoxy modification. Also, optionally phosphodiester or phosphothioate backbone"
XX US6090626-A.
XX PN 18-JUL-2000.
XX PD 28-AUG-1998; 98US-00143214.
XX PF 31-MAY-1994; 94US-00250856.
PR 31-MAY-1995; 95WO-US007111.
PR 26-NOV-1996; 96US-00756806.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Boggs RT, Monia BP;
XX WPI; 2000-531424/48.
XX Antisense oligonucleotides targeted to nucleic acid molecule encoding human raf useful for diagnosis, treatment of raf-associated cell proliferative conditions such as cancer, psoriasis or blood vessel restenosis.
XX Claim 31; Col 10; 31pp; English.
XX c-raf is a serine-threonine-specific protein kinase and is thought to play a fundamental role in signal transduction, and cell proliferation control. The present sequence is an antisense oligonucleotide. This sequence is targeted to human c-raf gene, resulting in c-raf expression inhibition. The present sequence may be useful for treating and raf-associated cell hyperproliferation conditions such as cancer, hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis, atherosclerosis and smooth muscle cell proliferation in blood vessels e.g. stenosis or restenosis following angioplasty. Also, the present

CC sequence may be useful for treating inflammatory disorders such as tissue
CC graft rejection, endotoxin shock and glomerular nephritis
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 129
AAD44740/c
ID AAD44740 standard; DNA; 20 BP.
XX
AC AAD44740;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human c-raf kinase antisense oligonucleotide ISIS #7853.
XX
KW Human; raf; hyperproliferation; neovascularisation; ocular angiogenesis;
KW therapy; cancer; cytostatic; anti-angiogenic; vascular; ophthalmological;
KW antisense; phosphorothioate backbone; c-raf kinase; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
FT modified_base 10..20 /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-O-methyl nucleotides"
XX
PN US6410518-B1.
XX
PD 25-JUN-2002.
XX
PF 18-FEB-2000; 2000US-00506073.
XX
PR 31-MAY-1994; 94US-00250856.
PR 31-MAY-1995; 95WO-US007111.
PR 26-NOV-1996; 96US-00756806.
PR 07-JUL-1997; 97US-00888982.
PR 06-JUL-1998; 98WO-US013961.
PR 28-AUG-1998; 98US-00143214.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP;
XX
DR WPI; 2002-597918/64.
XX
PT Treating cancer, angiogenesis or neovascularization by administering
PT antisense oligonucleotides targeted to human raf sequences.
XX
PS Disclosure; Col 14; 41pp; English.
XX
CC The present invention relates to novel antisense oligonucleotides which
CC are targeted to nucleic acids encoding human raf proteins and capable of
CC inhibiting raf expression. The invention also relates to methods of
CC inhibiting hyperproliferation of cells which involves contacting the
CC hyperproliferating cells with a therapeutically effective amount of an
CC oligonucleotide of the invention. The method is useful for treating
CC cancer, angiogenesis or neovascularisation, especially ocular
CC angiogenesis or neovascularisation. The present DNA sequence is an

CC antisense oligonucleotide targeted to human c-raf kinase
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 130
ACD42099/c
ID ACD42099 standard; DNA; 20 BP.
XX
AC ACD42099;
XX
DT 05-SEP-2003 (first entry)
XX
DE Antisense oligonucleotide targeting human c-raf, ISIS7853.
XX
KW Human; ss; antisense; c-raf; a-raf; b-raf; protein kinase; cancer;
KW signal transduction; cell proliferation; lung carcinoma; cytostatic;
KW antisense gene therapy; chemotherapeutic agent; angiogenesis;
KW hyperproliferative condition; neovascularisation; ocular angiogenesis.
XX
OS Homo sapiens.
XX
PN US2003032607-A1.
XX
PD 13-FEB-2003.
XX
PF 25-JAN-2002; 2002US-00057550.
XX
PR 31-MAY-1994; 94US-00250856.
PR 31-MAY-1995; 95WO-US007111.
PR 26-NOV-1996; 96US-00756806.
PR 07-JUL-1997; 97US-00888982.
PR 06-JUL-1998; 98WO-US013961.
PR 28-AUG-1998; 98US-00143214.
PR 18-FEB-2000; 2000US-00506073.
XX
PA (MONI/) MONIA B P.
XX
PI Monia BP;
XX
DR WPI; 2003-503332/47.
XX
PT Novel antisense oligonucleotide which is targeted to mRNA encoding human
PT raf and which is capable of inhibiting raf expression, useful for
PT treating or preventing hyperproliferative conditions such as cancer;
XX
PS Disclosure; Page 8; 42pp; English.
XX
CC The invention relates to an oligonucleotide 8-50 nucleotides in length
CC which is targeted to mRNA encoding human c-raf, a-raf or b-raf (raf is a
CC protein kinase playing a regulatory role in signal transduction,
CC regulating cell proliferation and has been implicated in lung carcinoma),
CC and which is capable of inhibiting raf expression. Also included is a
CC composition comprising the oligonucleotide and a pharmaceutically
CC acceptable carrier. The antisense oligonucleotide is useful for
CC inhibiting the expression of human raf in human cells or tissues, by
CC contacting the human cells or tissues with the oligo. The oligo, is also
CC is useful for treating or preventing a disease or condition associated
CC with the expression of raf by administering it in combination with a
CC chemotherapeutic agent to a human or cells of the human, where the
CC expression of raf is abnormal expression, and the condition is a
CC hyperproliferative condition such as cancer, angiogenesis or
CC neovascularisation (preferably ocular angiogenesis or
CC neovascularisation). The oligo, is also useful for inhibiting
CC hyperproliferation of cells. The oligos, are also useful as tools, for

CC example for detecting and determining the role of raf expression in
CC various cell functions and physiological processes and conditions and for
CC diagnosing conditions associated with raf expression and for research
CC purposes. The present sequence is an antisense oligonucleotide targeting
CC a human raf mRNA
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 131
ACA61359/c
ID ACA61359 standard; DNA; 20 BP.
XX
AC ACA61359;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human c-raf mRNA antisense oligonucleotide #7.
XX
KW Human; c-raf; antisense; ss; nuclease inhibitor; gene therapy; AIDS;
KW bacterial infection; viral infection; protozoan infection;
KW abnormal cell proliferation; tumour formation; atherosclerosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = phosphorothioate backbone. Optionally 10-
FT 20 are 2'-O-methyl nucleotides"
XX
PN US2003004325-A1.
XX
PD 02-JAN-2003.
XX
PF 28-NOV-2001; 2001US-00996263.
XX
PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 11-JAN-1991; 91WO-US000243.
PR 12-AUG-1991; 91WO-US005720.
PR 24-DEC-1991; 91US-00814961.
PR 05-MAR-1992; 92US-00835932.
PR 01-JUL-1992; 92US-00854634.
PR 23-DEC-1992; 92WO-US011339.
PR 21-JUN-1994; 94US-00244993.
PR 06-JUN-1995; 95US-00471973.
PR 17-AUG-1998; 98US-00135202.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Kawasaki AM;
XX
XX WPI; 2003-438873/41.
XX
PT New nuclease resistant compounds, useful as therapeutics, diagnostic
PT agents, or research reagents, or for treating an organism with a disease
PT associated with the undesired production of a protein, e.g. bacterial
PT infections or AIDS.
XX
PS Example 31; Page 29; 50pp; English.
XX
CC The invention relates to a nuclease resistant compound that hybridises

CC with RNA or DNA, comprising covalently-bound nucleosides that
CC individually include a ribose of deoxyribose sugar portion and a base
CC portion. The nuclease resistant compounds are useful as therapeutics,
CC diagnostic agents, or research reagents. The compounds are also useful
CC for modulating the activity of an RNA or DNA molecule, or for treating an
CC organism with a disease associated with the undesired production of a
CC protein, e.g. bacterial, viral or protozoan infections, AIDS, abnormal
CC cell proliferation and tumour formation, or atherosclerosis. The present
CC sequence represents the human c-raf mRNA antisense oligonucleotide #7
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 132
ADD44696/c
ID ADD44696 standard; DNA; 20 BP.
XX
AC ADD44696;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human c-Raf antisense oligonucleotide #7.
XX
KW Human; ss; antisense; c-Raf; virucide; anti-HIV; antiarteriosclerotic;
KW cytostatic; 2'-fluoro substituent; AIDS; atherosclerosis; cancer.
XX
OS Homo sapiens.
OS US2003187240-A1.
XX
PD 02-OCT-2003.
XX
PF 28-JAN-2003; 2003US-00352586.
XX
PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 05-MAR-1992; 92US-00835932.
PR 06-JUN-1995; 95US-00468037.
PR 02-SEP-1999; 99US-00389283.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Kawasaki AM;
XX
XX WPI; 2003-831271/77.
XX
PT Modified oligonucleotides useful as therapeutics, diagnostics and
PT research agents comprises several covalently bound nucleosides joined by
PT internucleoside linkages.
XX
PS Example 31; SEQ ID NO 13; 48pp; English.
XX
CC The invention relates to a modified oligonucleotide comprising several
CC covalently bound nucleosides including a ribose or deoxyribose sugar
CC portion and a base portion. The nucleosides are joined together by
CC internucleoside linkages such that the base portion of the nucleosides
CC form a mixed base sequence. At least one of the nucleosides includes a
CC modified ribofuranosyl moiety bearing a 2'-fluoro substituent. The
CC antisense oligonucleotides of the invention are useful as therapeutics,
CC diagnostics and research agents e.g. for the treatment of various viruses
CC (e.g. AIDS), for modulating the production of proteins by an organism,
CC treating an organism having a disease involving an undesired production
CC of a protein (e.g. atherosclerosis, cancer), detecting the presence or
CC absence of abnormal RNA molecules, or abnormal or inappropriate
CC expression of normal RNA molecules in organisms or cells, and for the

CC selective binding of RNA for use as research reagents and diagnostic
CC agents. The compounds have improved stability to enzymatic degradation
CC with various intracellular and extracellular nucleases, and improved
CC ability to bind to a specific DNA or RNA with fidelity compared to wild-
CC type DNA-DNA and RNA-DNA duplexes and phosphorus-modified oligonucleotide
CC duplexes containing methylphosphonates, phosphoramidates and phosphate
CC triesters. The present sequence is an antisense oligonucleotide of the
CC invention targeting human c-Raf.
XX
SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
|||
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 133
AAF03299/c
ID AAF03299 standard; DNA; 17 BP.

XX AAF03299;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1594.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
KW Homo sapiens.

OS
XX WO2000061729-A2.

PN 19-OCT-2000.

XX 11-APR-2000; 2000WO-US009721.

PF 12-APR-1999; 99US-0129390P.

PR (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;

PI WPI; 2000-647423/62.

DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.

PT Claim 37; Page 92; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 1 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAGCCA 1431
|||
Db 17 CAACTTCAAAAAGCCA 1

RESULT 134
AAF03298/c
ID AAF03298 standard; DNA; 17 BP.

XX AAF03298;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1593.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX Homo sapiens.

OS WO2000061729-A2.

PN 19-OCT-2000.

XX 11-APR-2000; 2000WO-US009721.

PF 12-APR-1999; 99US-0129390P.

PR (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;

PI WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.

XX Claim 37; Page 92; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1417 ACTTCAAAAAGCCAAG 1433
|||
Db 17 ACTTCAAAAAGCCAAG 1

RESULT 135
AA10583/c
ID AA10583 standard; DNA; 18 BP.

XX AA10583;

DT 29-JUN-2000 (first entry)

DE Smad2 antisense oligonucleotide sequence #36 (ISIS# 27813).

XX Smad2; MADH2; MADR2; hMAD2; JV18-1; transcription factor; inflammation;
KW chromosome 18q21; antisense compound; treat; prevent; infection; tumour;
KW diagnostic reagent; research reagent; ss; cancer.
XX Synthetic.

PN US6037142-A.
 XX 14-MAR-2000.
 PD 23-FEB-1999; 99US-00255912.
 XX 23-FEB-1999; 99US-00255912.
 PF (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowsert LM;
 PI WPI; 2000-269886/23.
 DR New antisense compound that inhibits human Smad2, useful e.g. for
 XX treating or preventing infection, inflammation and tumors.
 PT Claim 11; Col 39; 31pp; English.
 PS This sequence represents an antisense nucleotide sequence targeting human
 XX Smad2. Smad2 is also known as MADH2, MADR2, hMAD2 and JVL8-1, and is a
 CC member of a subgroup of Smad family transcription factors which are
 CC cytosolic proteins regulated by transforming growth factor-beta (TGF-
 CC beta) and activins. Smads exist as monomers in unstimulated cells as homo
 CC - or heterodimerise and translocate to the nucleus and activate target
 CC gene transcription upon ligand binding. The Smad2 gene is located on
 CC chromosome 18q21. The invention relates to antisense compounds (see
 CC AAA10548-A10587) targeted to the Smad2 nucleotide sequence. The antisense
 CC oligonucleotide sequences inhibit Smad2 expression by hybridising to DNA
 CC or RNA. The antisense nucleotides are used to treat or prevent diseases
 CC associated with expression of Smad2, e.g. infection, inflammation and
 CC tumours. The oligonucleotides can also be used as diagnostic or research
 CC reagents
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 84;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1557 TGAATGGACCTCTCCAG 1573
 DB 18 TGAATGGACCTCTACAG 2
 RESULT 136
 AAZ70696/C
 ID AAZ70696 standard; DNA; 18 BP.
 AC AAZ70696;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker upstream amplification primer SEQ ID NO:5052.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB0000822.
 XX 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX (GEST) GENSET.
 PA

XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.
 PT Claim 8; Page 1308; 2745pp; English.
 PS AAZ65654 to AAZ69578 represent human biallelic markers from the present
 XX invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 18 BP; 1 A; 8 C; 0 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 84;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1469 AGAGGAGAGAGAGGAA 1485
 DB 17 AGAGGAGAGAGATGGAA 1
 RESULT 137
 AAF53136
 ID AAF53136 standard; DNA; 15 BP.
 XX AAF53136;
 AC 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #4096.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 PD 21-JUN-2000; 2000WO-AU0000693.
 XX 21-JUN-1999; 99US-0140345P.
 PR (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 87; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1395 GGGGGCCGCAAGAAC 1409
Db 1 GGGGGCCGCAAGAAC 15

RESULT 138

AAAX22495/C
ID AAX22495 standard; RNA; 18 BP.

XX AAX22495;

XX 25-MAR-2003 (revised)

DT 21-MAY-1999 (first entry)

XX Streptomyces sp. est gene RBS RNA fragment.

XX Xylanase; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin; ds.

XX Streptomyces sp.

XX US5871730-A.

XX 16-FEB-1999.

XX 29-JUL-1994; 94US-00282197.

XX 29-JUL-1994; 94US-00282197.

XX (UYSH) UNIV SHERBROOKE.

XX Beaulieu C, Brzezinski R, Dery CV;

XX WPI; 1996-141348/14.

XX New acidophilic and thermostable xylanase enzymes from Actinomadura sp.
PT FC7 - useful for treating plant biomass, especially paper and wood pulp,
PT to degrade hemicellulose and hydrolyse xylan.

XX Example 7; Fig 7; 60pp; English.

XX This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high

CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of a
CC large group of hemicellulase enzymes and function by cutting the beta-1,4
CC bonds within the xylosic chain of xylan (a polymer of D-xylose residues
CC that is a major constituent of hemicellulose). This means that they may
CC be used in the paper and pulp industry to improve the efficiency of the
CC bleaching process by degrading the structure of the material. XYL I and
CC XYL II may also be used to treat feed, by degrading a substrate with a
CC high beta-glucan or cellulose content. XYL I and XYL II retain their
CC activity at high temperatures (e.g. 70 deg. C) and at low pHs (e.g. 4.0).
CC conditions which tend to denature most known xylanases. Enzymes that
CC remain active in these conditions may be used in industrial processes
CC that are carried out at high temperature and low pH to speed up other,
CC non-enzymatic reactions, minimising costs, energy requirements, and the
CC risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage. NOTE: This patent is an
CC equivalent to FI9503640. (Updated on 25-MAR-2003 to correct DR field.)

XX Sequence 18 BP; 6 A; 4 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 689 CATGACTGTGTCCTTCA 706
Db 18 CATGGCTGTGCCCTTCA 1

RESULT 139

AAV00348/C

ID AAV00348 standard; DNA; 18 BP.

XX AAV00348;

XX 23-APR-1998 (first entry)

DE Insecticidal gene sequence modification oligonucleotide BTK53.

XX Insecticidal protein; Bacillus thuringiensis; monocotyledonous plant;
KW structural gene; maize; CryI(b); CryIIb; ss.

XX Synthetic.

OS Bacillus thuringiensis.

XX US5689052-A.

XX 18-NOV-1997.

XX 19-SEP-1995; 95US-00530492.

XX 22-DEC-1993; 93US-00172333.

XX (MONS) MONSANTO CO.

XX Sanders PR, Brown SM, Dean DA, Fromm ME;

XX WPI; 1998-008070/01.

XX Genes encoding insecticidal proteins of Bacillus thuringiensis - modified
PT to enhance expression in monocotyledonous plants.

XX Example 1; Col 16; 86pp; English.

XX The present sequence represents an oligonucleotide used in the present
CC invention describing new structural genes capable of being expressed in a
CC monocotyledonous plant. The new genes comprise modified nucleotide
CC sequences which encode insecticidal proteins of Bacillus thuringiensis.

CC The genes have been modified to reduce the usage of codons that are rare
CC or semi-rare in monocotyledon DNA, thereby increasing transformation
CC efficiency and/or increasing accumulation of the insecticidal protein in
CC monocotyledon tissues
XX
SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 646 ATGGTGACGGCGTGGAG 663
Db 18 ATGGTGGCGGCGTGGAG 1

RESULT 140
AAZ94539
ID AAZ94539 standard; DNA; 18 BP.
XX
AC AAZ94539;
XX
DT 18-JUL-2000 (first entry)
DE Human cytokine receptor zalphall sense PCR primer ZC19954.
XX
KW Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KW signal transduction; growth factor; cancer; tumour; infection;
KW gene therapy; diagnosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200017235-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US022149.
XX
PR 23-SEP-1998; 98US-00159254.
PR 09-MAR-1999; 99US-00265117.
PR 06-JUL-1999; 99US-00347930.
XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
XX WPI; 2000-292825/25.
DR
XX Novel nucleic acid encoding zalphall polypeptide, useful for treating
PT e.g. viral infection or tumors, and for identifying ligands that
PT stimulate cell proliferation.
XX
PS Example 3; Page 155; 190pp; English.

XX
CC The present sequence is that of oligonucleotide ZC19954, used as sense
CC primer in the PCR based mapping of the human zalphall gene to the 16p11.1
CC region of chromosome 16. Zalphall (see also AAY79312) is a novel class I
CC cytokine receptor that may be involved in an apoptotic cellular pathway,
CC or is a cell-cell signalling molecule, growth factor receptor, or
CC extracellular matrix associated protein with growth factor hormone
CC activity. The invention provides zalphall polypeptides, polynucleotides
CC and antibodies, and methods for their use in the treatment and diagnosis
CC of conditions associated with altered zalphall expression or activity
XX
SQ Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATGGGCTGGGGCCTGC 528
Db 1 ACTGGCTGGGGACTGC 18

RESULT 141
AAF73266/C
ID AAF73266 standard; DNA; 18 BP.
XX
AC AAF73266;
XX
DT 26-APR-2001 (first entry)
DE Oligonucleotide #57.
XX
KW CryIA; transgenic; crystal; toxin; insecticide; ss.
XX
OS Synthetic.
XX
PN US6180774-B1.
XX
PD 30-JAN-2001.
XX
PF 05-AUG-1997; 97US-00906517.
XX
PR 22-DEC-1993; 93US-00172333.
PR 19-SEP-1995; 95US-00530492.
XX
PA (MONS) MONSANTO CO.
XX
PI Brown SM, Dean DA, Fromm ME, Sanders PR;
XX
DR WPI; 2001-190861/19.
XX
PT Novel nucleic acids, useful for transgenic plant production which is
PT capable of expressing increased levels of desired proteins.
XX
PS Example 1; Col 16; 81pp; English.

XX
CC The present invention relates to nucleotides 669-1348 of a
CC B.thuringiensis CryIA(b). The invention is useful for transgenic plant
CC production, e.g. maize, capable of expressing increased amount of
CC transgenic protein, e.g. crystal protein toxin gene of Bacillus
CC thuringiensis
XX
SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 646 ATGGTGACGGCGTGGAG 663
Db 18 ATGGTGGCGGCGTGGAG 1

RESULT 142
AAS20658
ID AAS20658 standard; DNA; 18 BP.
XX
AC AAS20658;
XX
DT 09-APR-2002 (first entry)
DE Human zalphall receptor sequencing primer ZC19954.
XX
KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; sequencing primer; ss.
XX
OS Homo sapiens.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.

CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
CC that stimulate the proliferation and/or development of haematopoietic,
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
CC in identifying a region of the genome associated with human disease
CC states. Zalphall protein is useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. The present sequence is
CC a primer used for sequence analysis of human MPL-Zalphall chimera. This
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGGCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 145
AAC72366
ID AAC72366 standard; DNA; 17 BP.
XX
AC AAC72366;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #1464.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1237 CACCTGGGGTCCAAAC 1252
Db 1 CAGCTGGGGTCCAAAC 16

RESULT 147
AAF03297/c
ID AAF03297 standard; DNA; 17 BP.
XX
AC AAF03297;
XX

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1237 CACCTGGGGTCCAAAC 1252
Db 1 CAGCTGGGGTCCAAAC 16

RESULT 146
AAC72375
ID AAC72375 standard; DNA; 17 BP.
XX
AC AAC72375;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #1470.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1237 CACCTGGGGTCCAAAC 1252
Db 1 CAGCTGGGGTCCAAAC 16

RESULT 147
AAF03297/c
ID AAF03297 standard; DNA; 17 BP.
XX
AC AAF03297;
XX

DT 16-FEB-2001 (first entry)
XX Hammerhead ribozyme substrate #1592.
DE
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX Homo sapiens.
OS
XX WO200061729-A2.
PN
XX 19-OCT-2000.
PD
XX 11-APR-2000; 2000WO-US009721.
PF
XX 12-APR-1999; 99US-0129390P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 92; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
PI Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 92; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;
QY 1418 CTTCAAAAAGCCAAG 1433
DB 17 CTTCAATAAGCCAAG 2
RESULT 148
AAFO3300/C
ID AAF03300 standard; DNA; 17 BP.
XX
AC AAF03300;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1595.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI
XX WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 92; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 4 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;
QY 1415 CAACTTCAAAAAGGCC 1430
DB 16 CAACTTCAATAAGGCC 1
RESULT 149
ABK03667/C
ID ABK03667 standard; RNA; 17 BP.
XX
AC ABK03667;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Antibody #16.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNase; inozyme; G-cleaver; ambrzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;

XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
XX
XX Claim 30; Page 166; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with an RNA motif) or a
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1119 TTGGACCAGATTTC A 1134
Db 16 TTGGACCAGATTGCA 1
|||||

RESULT 150
ABK03088/C
ID ABK03088 standard; RNA; 17 BP.
XX
XX AC ABK03088;
XX
XX 12-MAR-2002 (first entry)
XX
XX DE Human CD20 Inozyme #39.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW

Parkinson's disease; ataxia; Huntington's disease;
 Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 Homo sapiens.
 Synthetic.
 WO200159103-A2.
 16-AUG-2001.
 09-FEB-2001; 2001WO-US004273.
 11-FEB-2000; 2000US-0181797P.
 28-FEB-2000; 2000US-0185516P.
 06-MAR-2000; 2000US-0187128P.
 (RIBO-) RIBOZYME PHARM INC.
 (BLAT/) BLATT L.
 (MCSW/) MCSWIGGEN J.
 (CHOW/) CHOWRIRA B M.
 Blatt L, Mcswiggen J, Chowrira BM;
 WPI; 2001-607195/69.
 Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
 Claim 30; Page 146; 200pp; English.
 The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention
 Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 0.9%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1119 TTTGGACCAGATTTC A 1134
 |||||
 DB 17 TTTGGACCAGATTGCA 2

CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 512 TTGGGCTGGGGCCTG 527
Db 17 TTGGGCTGGGGCCTG 2
RESULT 152
ID ABN00980/c
AC ABN00980 standard; DNA; 17 BP.
XX
AC ABN00980;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:972.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 972; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration

RESULT 151
ID ABN00979/c
XX
AC ABN00979 standard; DNA; 17 BP.
XX
AC ABN00979;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:971.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 971; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCCTG 527
Db 16 TTGGGCTTGGGGCCTG 1

RESULT 153
ABQ64004/C
ID ABQ64004 standard; DNA; 17 BP.

XX AC ABQ64004;

XX DT 20-AUG-2002 (first entry)

XX DE Human KTOM1a portion (ABQ63232) probe # 717.

XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX OS Homo sapiens.

XX PN WO200224750-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-US029656.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 28-AUG-2001; 2001US-0315676P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhang J;

XX DR WPI; 2002-479509/51.

XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
XX PT acids encoding the protein, useful for treating subjects having defects
XX PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
XX PT e.g., liver or bone.

PS Example 2; Page 251; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human
XX KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
XX invention has cytostatic activity. The nucleotide may have a use in gene
XX therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
XX monitor a disease caused by altered expression of human KTOM1.

XX Compositions comprising the nucleic acids, proteins or antibodies may be
XX used to treat subjects having defects in KTOM1 which can manifest as
XX cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
XX heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
XX function. The sequence represents a probe used in the invention to scan
XX the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCAAACGCAGGCGATT 1262

Db 16 CCAAATGCAGGCGATT 1

RESULT 154
ABQ64003/C
ID ABQ64003 standard; DNA; 17 BP.

XX AC ABQ64003;

XX DT 20-AUG-2002 (first entry)

XX DE Human KTOM1a portion (ABQ63232) probe # 716.

XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX OS Homo sapiens.

XX PN WO200224750-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-US029656.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 28-AUG-2001; 2001US-0315676P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhang J;

XX DR WPI; 2002-479509/51.

XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
XX PT acids encoding the protein, useful for treating subjects having defects
XX PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
XX PT e.g., liver or bone.

XX Example 2; Page 251; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human

CC XTOM1 (kidney tumour overexpressed membrane) protein. The protein of the

CC invention has cytostatic activity. The nucleotide may have a use in gene

CC therapy. The XTOM1 nucleic acids may be used to diagnose, treat or

CC monitor a disease caused by altered expression of human XTOM1.

CC Compositions comprising the nucleic acids, proteins or antibodies may be

CC used to treat subjects having defects in XTOM1 which can manifest as

CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,

CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta

CC function. The sequence represents a probe used in the invention to scan

CC the nt 1-1001 portion of human XTOM1a (ABQ63232)

XX SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCAACGCGAGCGATT 1262

Db 17 CCAATGCGAGCGATT 2

RESULT 155

AAQ11746

ID AAQ11746 standard; DNA; 18 BP.

XX AC AAQ11746;

XX 24-OCT-2003 (revised)

DT 27-AUG-2003 (revised)

DT 02-AUG-1991 (first entry)

XX Target duplex from Herpes Simplex genome.

DE Triple helix; anti-sense therapy; switchback; polarity reversal; ds.

XX Viruses.

XX WO9106626-A.

XX 16-MAY-1991.

XX 23-OCT-1989; 89US-00425803.

XX 23-OCT-1989; 89US-00425803.

PR 29-MAR-1990; 90US-00502272.

PR 30-JUL-1990; 90US-00559958.

XX (GILE-) GILEAD SCI INC.

XX Froehler B, Toole JJ;

XX WPI; 1991-164176/22.

XX Oligo:nucleotide triple helix with double-helical nucleotide duplex -

PT useful in anti-sense therapy, to inhibit e.g. viral polymerase(s), or

PT interfere with binding factors to nucleic acids.

XX Disclosure; Fig 4A; 61pp; English.

XX The sequence is a target for novel oligonucleotides which comprise a 1st

CC sequence (S1), of at least 3 bases with 3'-5' or 5'-3' polar- ity,

CC coupled to a 2nd sequence (S2) of at least one base having the opposite

CC polarity. S1 and S2 are joined by 5'-5'; 3'-3'; base-5'; 5'-base; base-3',

CC ; or 3'-base linkages opt. through a linker. Other oligonucleotides

CC comprise a sequence (S3) of at least 3 bases en- riched in purine

CC residues, and a sequence (S4) of at least 3 bases enriched in

CC pyrimidines. Both types of oligos react with strands of target duplex DNA

CC to form a triplex. They are therefore useful in antisense therapy to

CC inactivate undesirable DNA or RNA and can also inhibit viral polymerases,

CC interfere with nucleic acid binding factors, induce interferon prodn.

CC etc. Oligos with a polarity reversal have better stability against

CC nuclease degradation. An oligo specific for the Herpes target duplex was

CC designed to have the formula: 5'-TTTTTTTNTTNT-3'-linker-3'-CCCC-5'.

CC It contains a region of inverted polarity but maintains the CT motif

CC throughout. It effects a crossover between the upper strand in which T

CC residues target the A-rich portion of the inverted polarity of the polyC

CC tract which targets the polyG region in the opposite strand. (Updated on

CC 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise

CC OS field)

XX SQ Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 1.1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCC 1468

Db 2 AAAAAGAGAAAGACCC 17

RESULT 156

AAQ68779/c

ID AAQ68779 standard; DNA; 18 BP.

XX AC AAQ68779;

XX 19-FEB-1995 (first entry)

XX CHA255 light chain CDR3 wild type coding sequence.

DE Polymerase chain reaction; primer; PCR; amplify; heavy; light; chain;

XX complementarity determining region; CDR; variable; constant; region;

KW monoclonal antibody; MAB; binding affinity; EDTA; DOTA; tumour; cancer;

KW colorectal; breast; metal chelate; hapten; ss.

XX Synthetic.

XX AU9350602-A.

XX 26-MAY-1994.

XX 10-NOV-1993; 93AU-00050602.

XX 12-NOV-1992; 92US-00975230.

XX (HYBR-) HYBRITECH INC.

XX Ahrweiler PM, Moore MD;

XX WPI; 1994-209063/26.

XX P-PSDB; AAR54177.

XX Polypeptide used in imaging and treatment of carcinomas and tumours -

PT comprising substd antibody CDR having binding affinity for metal chelate

PT of EDTA or DETA or analogues.

XX Claim 25; Fig 3B; 61pp; English.

XX The sequences given in AAQ68779-88 encode the wild type and mutagenised

CC versions of the complementarity determining region 3 (CDR3) of the

CC antibody designated CHA255 light chain. CHA255 is a murine monoclonal

CC antibody (MAB) which is capable of binding complexes. Mutagenesis of

CC these CDRs, causes the production of polypeptides with a particularly

CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3 of

CC the heavy chain, and CDR2 and -3 of the light chain were targeted for

CC mutagenesis. Five residues of both CDR1 and -3 of the CHA255 heavy chain,

CC five of seven residues of light chain CDR and six of nine light chain

CC CDR3 residues were specifically targeted for codon-based mutagenesis. The

CC mutagenised MAB's can be used in compositions for in vivo imaging of

CC malignant tissues or tumours. They are also useful for the treatment of

CC malignant tissues or tumours eg. colorectal or breast cancer. Both
CC methods involve the use of radionuclides which bind to metal chelates or
CC haptens which are specifically delivered to the target site by a
CC targetting molecule. CDR derived peptides may be used to construct bi-
CC functional antibodies having dual specificities, or as donor or
CC recipients of CDR sequences

XX
SQ Sequence 18 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 611 CCAGAGGGTGTGTAC 626
Db 18 CCAGAGGGTGTGTAC 3

RESULT 157
AAV57517/c
ID AAV57517 standard; DNA; 18 BP.
XX
AC AAV57517;
XX
DT 20-NOV-1998 (first entry)
XX
DE Zcytor7 cytokine receptor encoding cDNA amplifying outer nest primer.
XX
KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
KW agonist; cell proliferation; cell differentiation; renal disease; human;
KW neural disease; pancreatic disease; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9837193-A1.
XX
PD 27-AUG-1998.
XX
PF 18-FEB-1998; 98WO-US003029.
XX
PR 20-FEB-1997; 97US-00803305.
PR 02-OCT-1997; 97US-00943087.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Lok S, Kho CJ, Jelmborg AC, Adams RL, Whitmore TE, Farrah TM;
XX WPI; 1998-480798/41.
XX
PT Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for
PT treating renal, neural, pancreatic and prostatic diseases.
XX
PS Example 1; Page 62; 72pp; English.
XX
CC Sequences shown in AAV57517 to AAV57524 represent primers used for the
CC PCR amplification of the cDNA encoding the Zcytor7 cytokine receptor.
CC Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of
CC the type 2 cytokine receptor family (CRF2). An expression vector
CC containing the Zcytor polynucleotide, operably linked to transcription
CC promoter, a sequence encoding a transmembrane and intracellular domain,
CC or both, and a transcriptional terminator can be used to transform host
CC cells for the recombinant production of the polypeptide. The sequences
CC can be used to study the Zcytor7 gene and to isolate ligands binding to
CC it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate
CC or nervous tissue. Agonists of Zcytor7 can be used to stimulate
CC proliferation and differentiation of cell in these organs. The
CC antagonists and agonists can also be used in the treatment of renal,
CC neural, pancreatic and prostate diseases

XX
SQ Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
Db 17 AAAGAGAAACCCAG 2

RESULT 158
AAV52697
ID AAV52697 standard; DNA; 18 BP.
XX
AC AAV52697;
XX
DT 30-JUN-1999 (first entry)
XX
DE Human genome biallelic marker primer 65.
XX
KW Biallelic marker; human; high density disequilibrium map; disease; trait;
KW identification; Alzheimer's disease; drug response; drug efficacy;
KW drug toxicity; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9904038-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-IB001193.
XX
PR 18-JUL-1997; 97EP-00401740.
PR 21-APR-1998; 98US-0082614P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Tchoumakov I;
XX WPI; 1999-132278/11.
XX
PT Production of biallelic markers - by obtaining a genomic DNA library;
PT determining the order and sequence of DNA fragments and identifying
PT nucleotides which vary between individuals.
XX
PS Example 7; Page 212; 288pp; English.
XX
CC This invention describes a novel method for obtaining a set of biallelic
CC markers represented in AAV52533-X52632 and AAV52833-X52843 for use in
CC constructing a high density equilibrium map of the human genome. The
CC method involves (a) obtaining a nucleic acid library comprising genomic
CC DNA fragments comprising the full genome or a portion (b) determining the
CC order of genomic DNA fragments in the genome, (c) determining the
CC sequence of selected regions of the genomic DNA fragments and (d)
CC identifying nucleotides in the genomic DNA fragments which vary between
CC individuals, thereby defining a set of biallelic markers. The methods can
CC be used for identifying traits such as disease (e.g. Alzheimer's
CC disease), drug response, drug efficacy and drug toxicity. They can be
CC used for selecting an individual for inclusion in a clinical trial. The
CC method is used to map the position of genes in a genome (preferably the
CC human genome). The sequences described in AAV52633-X52832 and AAV52844-
CC X52868 represent primers used in the method of the invention

XX
SQ Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAG 1472
Db 1 AGAGAAAGAACCCAGAG 16

XX OS Homo sapiens.
XX XX
PN WO9954500-A2.
XX XX
PD 28-OCT-1999.
XX XX
PF 21-APR-1999; 99WO-IB000822.
XX XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX (GEST) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
XX PI
XX DR
XX WO2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1105; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 1 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTCTGGGTCTCTG 16
|||||
Db 1 ATGTCTGGGTCTCTG 16
RESULT 161
AAZ74823
ID AAZ74823 standard; DNA; 18 BP.
XX
AC AAZ74823;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9179.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.

RESULT 159
AAA49365
ID AAA49365 standard; DNA; 18 BP.
XX
AC AAA49365;
XX
DT 25-SEP-2000 (first entry)
XX
DE Sequencing primer for Neisseria meningitidis Hsp70 gene.
XX
KW Hsp70; Hsp60; heat shock protein; immunogen; immunity; vaccine;
KW detection; Neisseria meningitidis; Aspergillus fumigatus;
KW Candida glabrata; primer; ss.
XX
OS Synthetic.
XX
PN WO200034465-A2.
XX
PD 15-JUN-2000.
XX
PF 01-DEC-1999; 99WO-CA001152.
XX
PR 08-DEC-1998; 98US-00207388.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA Wisniewski J;
XX
PI
XX WPI; 2000-423415/36.
XX Isolated nucleic acid molecule for eliciting immune response in mammal
PT encodes Neisseria meningitidis heat shock protein 70, Aspergillus
PT fumigatus Hsp60 and Candida glabrata Hsp60 polypeptide.
XX Example 3; Page 51; 118pp; English.
XX
CC The Hsp70 heat shock protein or fragments derived from Neisseria
CC meningitidis and the Hsp60 heat shock protein or fragments derived from
CC Aspergillus fumigatus or Candida glabrata can be used as immunogens to
CC give protective immunity from these microorganisms. Nucleotide sequences
CC encoding these proteins are useful for producing recombinant proteins for
CC immunizing an animal or as probes and/or primers to detect the
CC microorganisms in a biological sample. Two primers (AAA49360, AAA49361)
CC were used to clone the Hsp70 gene of Neisseria meningitidis. This primer
CC was then used to confirm the sequence of the cloned gene
XX
SQ Sequence 18 BP; 7 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 283 AAGCCAATGCTGAGGA 298
|||||
Db 2 AAGCCAATGCCGAGGA 17
RESULT 160
AAZ69746
ID AAZ69746 standard; DNA; 18 BP.
XX
AC AAZ69746;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4102.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX (GEST) GENSET.
PA Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX Claim 8; Page 2187; 2745pp; English.
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the generic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1457 AGAGAAAGACCCAGAG 1472
DB 1 AGAGAAAGACCCAGAG 16
RESULT 162
AAF53137
ID AAF53137 standard; DNA; 15 BP.
AC AAF53137;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4097.
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
OS WO200078341-A1.
XX PD 28-DEC-2000.
XX PN 21-JUN-2000; 2000WO-AU000693.
XX PF 21-JUN-1999; 99US-0140345P.
XX PR (MURD-) MURDOCH CHILDRENS RES INST.
XX PA Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.

PI Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 87; 201pp; English.
PS The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 GGGGCCGCAAGAAC 1409
DB 1 GGGGCCGCAAGAAC 14
RESULT 163
AAF53135
ID AAF53135 standard; DNA; 15 BP.
XX AAF53135;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4095.
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
OS WO200078341-A1.
XX PN 28-DEC-2000.
XX PD 21-JUN-2000; 2000WO-AU000693.
XX PF 21-JUN-1999; 99US-0140345P.
XX PR (MURD-) MURDOCH CHILDRENS RES INST.
XX PA Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 87; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1395 GGGGGCCGCAAGAA 1408

Db 2 GGGGGCCGCAAGAA 15

RESULT 164

ACC67627/c

ID ACC67627 standard; DNA; 17 BP.

XX ACC67627;

01-JUL-2003 (first entry)

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4874.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.

XX Mus musculus.

XX WO2003025176-A2.

XX 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

XX Disclosure; Page 600; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour

CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 3 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 AATGCTGAGGAGAT 301

Db 15 AATGCTGAGGAGAT 2

RESULT 165

AAAX69652

ID AAAX69652 standard; RNA; 17 BP.

XX AAAX69652;

XX 28-JUL-1999 (first entry)

DE Human flt1 VEGF receptor hammerhead ribozyme substrate #947.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

XX Homo sapiens.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 75; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAAX67275 to AAAX75752 represent specific examples
CC of nucleic acid molecules from the present invention

XX Sequence 17 BP; 5 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAACTT 482
DB 1 CAACUGCUUUGAAACUU 17

RESULT 166
AAX73006/c
ID AAX73006 standard; RNA; 17 BP.
XX
AC AAX73006;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #439.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 136; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 6 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGTC 34
DB 17 CTGCTGGTGTGCTGTC 1

RESULT 167
AAX62242

ID AAX62242 standard; RNA; 17 BP.
XX
AC AAX62242;
XX
DT 16-JUL-1999 (first entry)
XX
DE Granule bound starch synthase hammerhead substrate SEQ ID NO:117.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
PN WO9710328-A2.
XX
PD 20-MAR-1997.
XX
PF 12-JUL-1996; 96WO-US011689.
XX
PR 13-JUL-1995; 95US-0001135P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (DOWC) DOWELANCO.
XX
PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;
XX
DR WPI; 1997-202224/18.
XX
PT Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX
PS Claim 41; Page 73; 155pp; English.
XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.2e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 495 ACGGACATCGCCGTGAA 511
DB 1 AAGUACAUCGCCGUGAA 17

RESULT 168
AAA17513/c
ID AAA17513 standard; RNA; 17 BP.
XX
AC AAA17513;
XX
DT 19-JUN-2000 (first entry)
XX
DE Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:739.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
XX
PF 24-MAR-1999; 99WO-US006507.
XX
XX
PR 27-MAR-1998; 98US-0079678P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
DR
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PT
XX
XX Claim 53; Page 84; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17694 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 3 A; 7 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1375 ATTCTGAAGAGGAGGGA 1391
Db 17 ATTCTGAAGAGGAGGGA 1

RESULT 169
AAZ93921/c
ID AAZ93921 standard; DNA; 17 BP.
XX
AC AAZ93921;
XX
DT 25-SEP-2000 (first entry)

XX Primer (EPI/11RT) for amplifying EP-1 prostaglandin receptor sequence.
DE Prostaglandin; receptor; pulmonary system; glaucoma; identification;
XX allele; polymorphism; detection; prostanoid; FP; IP; DP; EP; TP; human;
KW ss.
KW
XX Synthetic.
OS
XX WO200029614-A1.
PN
XX
PD 25-MAY-2000.
XX
XX
PF 12-NOV-1998; 98WO-IB001803.
XX
XX
PR 12-NOV-1998; 98WO-IB001803.
XX
XX
PA (EURO-) EURONA MEDICAL AB.
XX
XX
PI Jonsson L, Lindstroem HR;
XX WPI; 2000-387820/33.
DR
XX
XX Assessing prostanoid response status in an individual suffering from
PT prostaglandin associated diseases such as pulmonary hypertension,
PT glaucoma or arteriosclerosis, comprises comparing polymorphic patterns.
XX
XX
PS Disclosure; Page 38; 57pp; English.
XX
XX The prostaglandin receptor family encompasses at least five classes of
CC receptors designated FP, EP, IP, DP and TP receptors which are classified
CC based on their sensitivity to the five primary prostanoids (F2alpha, E_2,
CC I_2, D_2 and TXA_2). EP receptors further comprise four subtypes,
CC designated EPI-4, which differ in their responses to various agonists and
CC antagonists. The receptors have also shown a degree of cross reactivity.
CC They may derive from a common ancestral gene. All of the receptors may
CC exist as allelic variants and these polymorphisms may have an affect on a
CC patients reaction to prostanoids. Detection of these polymorphisms may
CC identify patients at risk from toxic or abnormal responses to prostanoid
CC treatment. The prostaglandins play a role in the pulmonary system and in
CC glaucoma. Fourteen primers (See AAZ93918-293931) were used to amplify the
CC EP-1 prostaglandin receptor sequence. This primer corresponds to the 5'
CC region and nucleotides 1-12 of the EP-1 receptor sequence. Primers whose
CC designation include a "T" have the 29 base "tail sequence" given in
CC GENESEQ record AAZ93932 added to their 5' end
XX
SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTCTGCCCGCTGGTGCT 28
Db 17 CTGTGCCCGCTGCTGCT 1

RESULT 170
AAC61360/c
ID AAC61360 standard; DNA; 17 BP.
XX
XX AAC61360;
AC
XX
XX 30-JAN-2001 (first entry)
DT
XX
XX Human FP and EPI receptor genes PCR primer SEQ ID NO: 160.
DE
XX
XX Human; genetic polymorphism; disease diagnosis; treatment; cancer;
KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200056922-A2.
PN

XX 28-SEP-2000.
 XX
 PF 23-MAR-2000; 2000WO-GB001102.
 XX
 PR 23-MAR-1999; 99US-0126046P.
 PR 23-MAR-1999; 99WO-IB000497.
 PR 24-MAR-1999; 99US-0126243P.
 PR 23-DEC-1999; 99US-00471890.
 XX
 PA (GEMI-) GEMINI GENOMICS AB.
 XX
 PI Lindstrom PHR, Norberg LT, Jonsson L, Olaisson E, Sanders R;
 XX
 DR WPI; 2000-638268/61.
 XX
 PT Assessing disease status in individual by determining sequence(s) at one
 PT or more polymorphic positions within the human genes encoding the
 PT protein(s) involved in physiological pathway associated with treatment
 PT regime.
 XX
 PS Example 10; Page 101; 141pp; English.
 XX
 CC The present invention is related to methods for determining the
 CC polymorphic pattern of an individual and using the results to determine
 CC their risk of a number of diseases, including cancer, cardiovascular
 CC diseases, glaucoma and nervous system disorders such as depression and
 CC neurodegenerative diseases. In addition, the methods can be used to
 CC determine the effects of different types of treatment for individuals,
 CC and thus enables appropriate therapies to be prescribed. The PCR primers
 CC shown in sequences AAC61201-C61371 were all used to demonstrate the
 CC methods of the invention
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 CTCTGCCCGCTGGTCT 28
 Db 17 CTCTGCCCGCTGGTCT 1
 RESULT 171
 AAF02125/C
 ID AAF02125 standard; DNA; 17 BP.
 XX
 AC AAF02125;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #420.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 37; Page 65; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 49 CCTGAGAACACAGCCTG 65
 Db 17 CCTGAGAACACAGCCTG 1
 RESULT 172
 ABL46462
 ID ABL46462 standard; RNA; 17 BP.
 XX
 AC ABL46462;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID hammerhead ribozyme substrate oligonucleotide #95.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX
 DR WPI; 2001-550088/61.
 XX
 PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 PS Claim 4; Page 61; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 8 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGGAGC 1518
Db 1 AGCCAAGAGGAGGAGC 17

RESULT 177
ABN08675
ID ABN08675 standard; DNA; 17 BP.
XX
AC ABN08675;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8667.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 8667; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAG 1517
Db 1 AAGCCAAGAGGAGAG 17

RESULT 178
ABQ63445
ID ABQ63445 standard; DNA; 17 BP.
XX
AC ABQ63445;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 158.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PS Example 2; Page 178; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC Ktomi (kidney tumor overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The Ktomi nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human Ktomi.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in Ktomi which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human Ktomi (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1583 CCTGCTGAGTCCCTCAC 1599
Db 1 CCTGCTGACTCCACAC 17

RESULT 179
ABV79342
ID ABV79342 standard; DNA; 17 BP.
XX
AC ABV79342;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 588.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000563.
PR 30-JAN-2001; 2001WO-US000564.
PR 30-JAN-2001; 2001WO-US000565.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX

PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 140; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, are
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 8 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1456 AAGAGAAAGACCCAGAG 1472
Db 1 AAGAGGAAGACCTAGAG 17

RESULT 180
ABV79344
ID ABV79344 standard; DNA; 17 BP.
XX
AC ABV79344;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 590.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX

PA (ABOM-) ABOMICA INC.
XX Zhan J;
PI WPI; 2002-676582/73.
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX Example 2; Page 141; 718pp; English.
PS The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
SQ

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1458 GAGAAAGACCCAGAGGA 1474
Db 1 GAGGAAGACCTAGAGGA 17

RESULT 181
ABV79345
ID ABV79345 standard; DNA; 17 BP.
XX ABV79345;
AC
XX 03-JAN-2003 (first entry)
XX Human HTPL scanning oligonucleotide SEQ ID 591.
DE
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX Homo sapiens.
OS
XX EP1229046-A2.
PN
XX 07-AUG-2002.
PD
XX 28-JAN-2002; 2002EP-00001167.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.
XX (ABOM-) ABOMICA INC.
PA Zhan J;
XX WPI; 2002-676582/73.
PI Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
DR Example 2; Page 141; 718pp; English.
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
SQ

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1459 AGAAAGACCCAGAGGAG 1475
Db 1 AGGAAGACCTAGAGGAG 17

RESULT 182
ABV79343
ID ABV79343 standard; DNA; 17 BP.
XX ABV79343;
AC
XX 03-JAN-2003 (first entry)
XX Human HTPL scanning oligonucleotide SEQ ID 589.
DE
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX Homo sapiens.
OS
XX EP1229046-A2.
PN
XX 07-AUG-2002.
PD
XX 28-JAN-2002; 2002EP-00001167.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Zhan J;
PI
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 141; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAGG 1473
DB 1 AGAGGAAGACCTAGAGG 17

RESULT 183
ABK18013
ID ABK18013 standard; RNA; 17 BP.
XX
AC ABK18013;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 660.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnarary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX

PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
PI
XX WPI; 2002-082995/11.
DR
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 71; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 7 A; 4 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 298 AGATGACCAAGTACCAC 314
DB 1 AGAUGACCAAGGACGAC 17

RESULT 184
ABK18165
ID ABK18165 standard; RNA; 17 BP.
XX
AC ABK18165;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 812.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnarary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.

XX Homo sapiens.
 OS
 XX WO200188124-A2.
 PN
 XX
 XX
 PD
 XX 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX
 DR WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 PT
 XX
 PS Claim 4; Page 73; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 1.2e+02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 142 TCTGTTACTACTACGAC 158
 Db 1 UCCGUUACUACUAGAC 17
 RESULT 185
 ABN85838
 ID ABN85838 standard; DNA; 17 BP.
 XX
 AC ABN85838;
 XX
 DT 03-SEP-2002 (first entry)
 XX
 DE Related to Bombyx mori silk fibroin primer #38.
 XX
 KW Silk; fibroin; textile industry; PCR; primer; ss.
 XX

OS Unidentified.
 XX
 PN WO200240528-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 26-OCT-2001; 2001WO-CN001506.
 XX
 PR 26-OCT-2000; 2000CN-00125859.
 XX
 XX (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
 PA
 XX Lu C, Huang J, Zhao Y, Zhang F, Chen X;
 PI
 XX WPI; 2002-427084/45.
 DR
 XX Method for producing non-natural silk by Bombyx mori with modifying heavy
 PT and light chains of fibroin in natural silk by DNA recombination
 PT technology and protein engineering, applicable in sericulture and textile
 PT industry.
 XX
 PS Example 3; Page 18; 50pp; Chinese.
 XX
 CC This invention relates to a silk which constitutes recombinant Bombyx
 CC mori silk fibroin obtained by modification or variation at the heavy or
 CC light chains of the fibroin. The method is for producing non-natural
 CC silk, which is applicable in sericulture and textile industry. Such
 CC modified silk has improved performance. The present sequence is a primer
 CC related to the invention
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 800 CGGGATTGATGACGAGT 816
 Db 1 CAGGGTTGATGACGAGT 17
 RESULT 186
 ABL31482/C
 ID ABL31482 standard; DNA; 17 BP.
 XX
 AC ABL31482;
 XX
 DT 21-MAR-2002 (first entry)
 XX
 DE Human HLA genotyping oligonucleotide SEQ ID NO 971.
 XX
 KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 OS Homo sapiens.
 XX
 PN WO200192572-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-JP004662.
 XX
 PR 01-JUN-2000; 2000JP-00164798.
 XX
 XX (NISN) NISSHINBO IND INC.
 PA (SYST-) SYSTEM RES INC.
 PA
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 PI
 XX WPI; 2002-122074/16.
 DR
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when

PT transplanting between them.
XX
PS Claim 10; Page 277; 345pp; Japanese.
XX
CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 38 CACTCGGTGCATCCTGAG 54
Db 17 CACTCGGTGCAGCCTGTG 1
RESULT 187
ABK55737/C
ID ABK55737 standard; RNA; 17 BP.
XX
AC ABK55737;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #108.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 54; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 374 CAAGCAGATGCAGAGAT 390
Db 17 CAAACAGATACAGAGAT 1
RESULT 188
ABT21381/C
ID ABT21381 standard; DNA; 17 BP.
XX
AC ABT21381;
XX
DT 16-APR-2003 (first entry)
XX
DE Multiplex group PCR primer #128.
XX
KW Racing potential; horse; grandpaternal DNA; over-represented; breeding;
KW grandmother; performance; progeny horse; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200292851-A2.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-GB002273.
XX
PR 15-MAY-2001; 2001GB-00011886.
XX
PA (ANIM-) ANIMAL HEALTH TRUST.
PA (BRHO-) BRITISH HORSERACING BOARD.
XX
PI Binns MM, Swinburne JE;
XX
DR WPI; 2003-129314/12.
XX
PT Determining the racing potential of a horse comprises measuring whether
PT grandpaternal or grandmaternal DNA from the selected grandmother DNA is
PT over-represented in the genome of the horse.
XX
PS Example 2; Page 24; 49pp; English.
XX
CC The invention relates to a novel method for determining racing potential
CC of a horse. The method comprises measuring: whether grandpaternal DNA is
CC over-represented in the genome of the horse; or in the case where one of
CC the grandmothers was selected for breeding on the basis of racing
CC performance, whether grandmaternal DNA from the selected grandmother is
CC over-represented in the genome of the horse which indicates that the
CC horse has good racing potential. The method of the invention is useful
CC for determining the racing potential of a horse or for obtaining a
CC progeny horse with good racing potential. This polynucleotide sequence
CC represents a PCR primer used in the detection method of over-
CC representation of DNA from male grandparents of the invention
XX

SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 24 GTGCTGCTGCTCTCCAC 40
Db 17 GTCTGCTGCTCTCCAC 1
RESULT 189
ABZ65102
ID ABZ65102 standard; RNA; 17 BP.
XX
AC ABZ65102;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNzyme substrate #559.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
FN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 4; Page 143; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1315 ACAAGCGCATCTCGATC 1331
Db 1 ACAAGGGCAUCUGGAUC 17

RESULT 190
ABZ61604
ID ABZ61604 standard; RNA; 17 BP.
XX
AC ABZ61604;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNzyme target #395.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
FN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 118; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1296 GAGGACGAGACGACCC 1312
Db 1 GUGGACGAAUACGACCC 17
RESULT 191
ABZ61695
ID ABZ61695 standard; RNA; 17 BP.
XX
AC ABZ61695;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNzyme target #486.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2001; 2001US-0294140P.

XX 06-JUN-2001; 2001US-0296249P.

XX 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

XX treating cancer, modulates the expression of a nucleic acid encoding

XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 120; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX ABZ65530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention

XX Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

XX Query Match 0.9%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 64.7%; Pred. No. 1.2e+02;

XX Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

XX 658 TGGAGAGGCGCTTCTAC 674

XX 1 UGGAGGAUGCCUUCUAC 17

XX RESULT 192

XX ACD62482

XX ID ACD62482 standard; RNA; 17 BP.

XX AC ACD62482;

XX 23-SEP-2003 (first entry)

XX HCV minus strand DNazyme substrate sequence #569.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
XX amberyze; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MACE/) MACEJAK D.

XX (MCSW/) MCSWIGGEN J.

XX (MORR/) MORRISSEY D.

XX (PAVC/) PAVCO P.

XX (LEEP/) LEE P.

XX (DRAP/) DRAPER K.

XX (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

XX Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX Claim 1; Page 285; 387pp; English.
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberyzes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention

XX Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

XX Query Match 0.9%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 76.5%; Pred. No. 1.2e+02;

XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX 291 GCTGAGGAGATGACCAA 307

XX 1 GCTGAGGAGCUGGCCAA 17

XX RESULT 193

XX ACD60187/c

XX ID ACD60187 standard; RNA; 17 BP.

XX AC ACD60187;

XX 24-SEP-2003 (first entry)

XX HCV DNazyme substrate sequence #1709.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1267 AGGACGCCATCCTGAG 1283
1 AGGACCCCAACCCUGAG 17

Db

RESULT 195
ACD62411/C
ID ACD62411 standard; RNA; 17 BP.
XX AC ACD62411;
XX DT 23-SEP-2003 (first entry)
XX DE HCV minus strand DNAAzyme substrate sequence #554.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX KW RNA stability; RNA expression; RNA synthesis; antisense;
XX KW enzymatic nucleic acid; hammerhead ribozyme; DNAAzyme; inozyme; zinzyme;
XX KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX KW HBV reverse transcriptase; Enhancer I region; viral replication;
XX KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX KW virucide; antiinflammatory; substrate; ss.
XX OS Hepatitis C virus.
XX PN WO200281494-A1.
XX PD 17-OCT-2002.
XX PF 26-MAR-2002; 2002WO-US009187.
XX PR 26-MAR-2001; 2001US-00817879.
XX PR 08-JUN-2001; 2001US-00877478.
XX PR 08-JUN-2001; 2001US-0296876P.
XX PR 24-OCT-2001; 2001US-0335059P.
XX PR 05-DEC-2001; 2001US-0337055P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MACE/) MACEJAK D.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (MORR/) MORRISSEY D.
XX PA (PAVC/) PAVCO P.
XX PA (LEEP/) LEE P.
XX PA (DRAP/) DRAPER K.
XX PA (ROBE/) ROBERTS E.
XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX PS Claim 1; Page 284; 387pp; English.
XX CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAAzyme or minus strand DNAAzyme sequences disclosed in the present
CC invention
XX SQ Sequence 17 BP; 3 A; 2 C; 6 G; 0 T; 6 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 CAATATGACTAACCAGA 1170
17 CAATATGACTCCCCAGA 1

Db

RESULT 196
ACD51143/C
ID ACD51143 standard; RNA; 17 BP.
XX AC ACD51143;
XX DT 23-SEP-2003 (first entry)
XX DE HBV hammerhead ribozyme substrate sequence #405.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX KW RNA stability; RNA expression; RNA synthesis; antisense;
XX KW enzymatic nucleic acid; hammerhead ribozyme; DNAAzyme; inozyme; zinzyme;
XX KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX KW HBV reverse transcriptase; Enhancer I region; viral replication;
XX KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX KW virucide; antiinflammatory; substrate; ss.
XX OS Hepatitis B virus.
XX PN WO200281494-A1.
XX PD 17-OCT-2002.
XX PF 26-MAR-2002; 2002WO-US009187.
XX PR 26-MAR-2001; 2001US-00817879.
XX PR 08-JUN-2001; 2001US-00877478.
XX PR 08-JUN-2001; 2001US-0296876P.
XX PR 24-OCT-2001; 2001US-0335059P.
XX PR 05-DEC-2001; 2001US-0337055P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MACE/) MACEJAK D.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (MORR/) MORRISSEY D.
XX PA (PAVC/) PAVCO P.
XX PA (LEEP/) LEE P.
XX PA (DRAP/) DRAPER K.
XX PA (ROBE/) ROBERTS E.
XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.

XX Example 1; Page 144; 387pp; English.

PS The present invention relates to nucleic acid molecules which modulate

XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HBV

CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences

CC disclosed in the present invention

XX

SQ Sequence 17 BP; 1 A; 5 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 AGAAGCCAGAGCCAAA 1529

Db 17 AGAAGTCAGAGGCAAA 1

RESULT 197

ACD60202

ID ACD60202 standard; RNA; 17 BP.

XX

AC ACD60202;

XX

DT 24-SEP-2003 (first entry)

XX

DE HCV DNazyme substrate sequence #1724.

XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

KW RNA stability; RNA expression; RNA synthesis; antisense;

KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;

KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;

KW HBV reverse transcriptase; Enhancer I region; viral replication;

KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;

KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KW virucide; antiinflammatory; substrate; ss.

XX

OS Hepatitis C virus.

XX

PN WO200281494-A1.

XX

PD 17-OCT-2002.

XX

PF 26-MAR-2002; 2002WO-US009187.

XX

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-0087478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

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PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX

DR WPI; 2003-229207/22.

XX

PT Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX

PS Claim 1; Page 264; 387pp; English.

XX

CC The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HCV

CC DNazyme or minus strand DNazyme sequences disclosed in the present

CC invention

XX

SQ Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 70.6%; Pred. No. 1.2e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1153 CCAATATGACTAACCCAG 1169

Db 1 CCAUAUGACUCCCCAG 17

RESULT 198

ACC63240/C

ID ACC63240 standard; DNA; 17 BP.

XX

AC ACC63240;

XX

DT 01-JUL-2003 (first entry)

XX

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 487.

XX

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;

KW tumour suppression; tumour reversion; apoptosis; virus resistance;

KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;

KW schizophrania; ss.

XX

OS Mus musculus.

XX

PN WO2003025176-A2.

XX

PD 27-MAR-2003.

XX

PF 17-SEP-2002; 2002WO-IB004210.

XX

PR 17-SEP-2001; 2001FR-00011979.

XX

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX

DR WPI; 2003-333167/31.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 88; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 CTGCTCTCCCACTCGGTC 46
Db 17 CTGCTCTCCCACTCGATC 1

RESULT 199
ACC68438
ID ACC68438 standard; DNA; 17 BP.
XX
AC ACC68438;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5685.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 695; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of

CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1328 GATCTGCTCCTCTGACA 1344
Db 1 GATCTGCTCATTGACA 17

RESULT 200
ADB42595/c
ID ADB42595 standard; DNA; 17 BP.
XX
AC ADB42595;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2918.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 373; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 717 GAGTACTTCCCGAAGC 733
Db 17 GAGAACTTCCCGAGGATC 1

RESULT 201
ADB42646/C
ID ADB42646 standard; DNA; 17 BP.
XX
AC ADB42646;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2969.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 379; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 902 CTCCTATCTGGGATC 918
Db 17 CTTCTGTCTGGGATC 1

RESULT 202
ADC04842/C
ID ADC04842 standard; DNA; 17 BP.
XX
AC ADC04842;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Na/H exchanger-like protein 1 gene oligonucleotide #1289.
XX
KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHEP1; passive replacement therapy; vaccine; diagnosis.
XX
OS Homo sapiens.
XX
PN EP1273660-A2.
XX
PD 08-JAN-2003.
XX
PF 25-JAN-2002; 2002EP-00001160.
XX
PR 30-JAN-2001; 2001WO-US000666.
PR 23-MAY-2001; 2001US-00864761.
PR 21-DEC-2001; 2001US-0343331P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y;
XX
DR WPI; 2003-302724/30.
XX
PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHEP1.
XX
PS Example 2; SEQ ID NO 1329; 468pp; English.
XX
CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHEP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC spanning the sequence of the human NHEP1 gene (ADC03514).
XX
SQ Sequence 17 BP; 0 A; 11 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1381 AAGAGGAGGAGAGGGG 1397
Db 17 AGGAGGAGGAGAGGGG 1

```
RESULT 203
ADD80993/C
ID ADD80993 standard; DNA; 17 BP.
XX
AC ADD80993;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rabbit beta-globin fragment derived oligonucleotide #27.
XX
KW ss; oligonucleotide hybridisation potential; efficient hybridisation;
large array; minimum oligonucleotide synthesis; rabbit; beta-globin.
XX
OS Oryctolagus cuniculus.
XX
PN US2003054346-A1.
XX
PD 20-MAR-2003.
XX
PF 15-FEB-2001; 2001US-00784674.
XX
PR 10-FEB-1998; 98US-00021701.
XX
PA (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINC/) KINCAID R H.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX WPI; 2003-743746/70.
DR
XX
PT Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
PS Example 1; SEQ ID NO 66; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridize to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC rabbit beta-globin derived oligonucleotide sequence.
XX
SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTGGGGTCTCTGCC 19
Db 17 GTCTGGGGTCACTGCC 1

RESULT 204
AAF48241/C
ID AAF48241 standard; DNA; 15 BP.
XX
AC AAF48241;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1661.
XX
```

```
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO2000078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 55; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1376 TTCTGAAGAGGAGGG 1390
Db 15 TCCTGAAGAGGAGGG 1

RESULT 205
AAF45342
ID AAF45342 standard; DNA; 15 BP.
XX
AC AAF45342;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #181.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
```

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.
OS
XX WO200078341-A1.
PN
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU0000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
DR
XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 6; Page 35; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 0 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGCTGCTGCTGCTG 32
Db 1 CCGCTGCTGCTGCTG 15

RESULT 206
AAF49639
ID AAF49639 standard; DNA; 15 BP.
XX
AC AAF49639;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #599.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.
OS
XX WO200078341-A1.
PN
XX 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU0000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 64; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGC 1518
Db 1 CCATGGAGGAGAGC 15

RESULT 207
AAF49640
ID AAF49640 standard; DNA; 15 BP.
XX
AC AAF49640;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #600.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.
XX
PN WO200078341-A1.

XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wraight CJ, Werther GA, Edmondson SR;
 XX DR WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 8; Page 64; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX SQ Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1505 CAAGGAGGAGAGCC 1519
 DB 1 CATGGAGGAGAGCC 15
 RESULT 208
 AAF49372/C
 ID AAF49372 standard; DNA; 15 BP.
 XX AC AAF49372;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #332.
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 28-DEC-2000.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wraight CJ, Werther GA, Edmondson SR;
 XX DR WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 8; Page 63; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX SQ Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1361 GGAAGAGTTCTCCGA 1375
 DB 15 GGAAGAGTTCTCCGA 1
 RESULT 209
 AAF52624
 ID AAF52624 standard; DNA; 15 BP.
 XX AC AAF52624;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #3584.
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;
PI XX
XX WPI; 2001-041421/05.
DR XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
PT XX
PS Example 8; Page 84; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1584 CTGCTGAGTCCCTCA 1598
Db 1 CTCCTGAGTCCCTCA 15
RESULT 210
AAF53134
ID AAF53134 standard; DNA; 15 BP.
XX
AC AAF53134;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #4094.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PD WO200078341-A1.
XX
PN 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
PI WPI; 2001-041421/05.
DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
PT XX
XX Example 8; Page 87; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1393 AGGGGGGCCGCAAGA 1407
Db 1 ACGGGGGCCGCAAGA 15
RESULT 211
AAF49638
ID AAF49638 standard; DNA; 15 BP.
XX
AC AAF49638;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #598.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
XX WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
PI WPI; 2001-041421/05.
DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT

PT inflammation.
XX Example 8; Page 64; 201pp; English.
PS
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 6 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1503 ACCAAGGAGGAGAG 1517
Db 1 ACCATGGAGGAGAG 15
RESULT 212
ABK81387
ID ABK81387 standard; DNA; 15 BP.
XX
AC ABK81387;
XX
DT 13-AUG-2002 (first entry)
XX
DE SCYA21 gene allele specific oligonucleotide primer #1.
XX
KW Small inducible cytokine subfamily A (Cys-Cys) member 21; SCYA21;
KW polymorphism; haplotype; immunological disorder; gene expression;
KW drug development; immunomodulator; allele specific oligonucleotide;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200232930-A2.
XX
PD 25-APR-2002.
XX
PF 09-OCT-2001; 2001WO-US046141.
XX
PR 19-OCT-2000; 2000US-0241622P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Russo DP;
XX
DR WPI; 2002-435528/46.
XX
PT New genetic variants comprising haplotypes of the small inducible
PT cytokine subfamily A, member 21 (SCYA21) gene, useful in improving the
PT efficiency of screening for drugs for treating immunological disorders or
PT for targeting SCYA21.
XX
PS Claim 14; Page 13; 56pp; English.
XX
CC The invention describes an isolated polynucleotide, which comprises genes
CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),
CC member 21 (SCYA21) gene. The polynucleotide comprises polymorphic sites
CC referred to as PS1-5 to designate the order in which they are located in

CC the gene. The polymorphisms and haplotypes of SCYA21 gene are useful for
CC validating whether SCYA21 is a suitable target for drugs to treat
CC immunological disorders and disorders associated with its abnormal
CC expression or function, screening for such drugs and reducing bias in
CC clinical trials of such drugs. Haplotype information would be useful in
CC improving the efficiency and output of several steps in the drug
CC discovery and development process, including target validation,
CC identifying lead compounds and early phase clinical trials. The methods
CC are useful in screening for compounds targeting SCYA21 to treat a
CC specific condition or disease predicted to be associated with SCYA21
CC activity, e.g. immunological disorders. This sequence represents an
CC allele specific oligonucleotide primer used to identify polymorphic sites
CC in the SCYA21 gene
XX
SQ Sequence 15 BP; 3 A; 3 C; 4 G; 4 T; 0 U; 1 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 401 TGAGGACTGTCCAGT 415
Db 1 TGAGGACTGTCCAYT 15
RESULT 213
AAQ96309/C
ID AAQ96309 standard; DNA; 16 BP.
XX
AC AAQ96309;
XX
DT 28-FEB-1996 (first entry)
XX
DE p53 gene hybridisation probe.
XX
KW p53 gene; hybridisation probe; detection; tumour; cancer;
KW chemoprevention; chemotherapy; ss.
XX
OS Synthetic.
XX
PN WO9519448-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-US0000657.
XX
PR 14-JAN-1994; 94US-00181664.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI Sidransky D;
XX
DR WPI; 1995-263876/34.
XX
PT Detection of a target neoplastic nucleic acid and treatment of tumours -
PT provides a rapid and accurate detection of mutant sequences.
XX
PS Example 1; Page 37; 126pp; English.
XX
CC AAQ96305-Q96363 are p53 gene hybridisation probes, used in the
CC development of a new method for the detection of mutant nucleotide
CC sequences associated with primary tumours. The method may be used to
CC screen high risk populations, and to monitor patients undergoing
CC chemoprevention or chemotherapy
XX
SQ Sequence 16 BP; 1 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 111 ATGGCGCAGACGAG 125
|||||

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB0000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 151965; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAA 1427
13 CAACTTCAAAAAA 1

RESULT 216
ABF45448/C
ID ABF45448 standard; DNA; 13 BP.

ABF45448;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 145445 for detecting SNP TSC0036625.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB0000713.

07-APR-2000; 2000DE-01019173.

```

Db      15 ATGGCGCAGACGOGG 1

RESULT 214
ABF45449
ID      ABF45449 standard; DNA; 13 BP.
XX
AC      ABF45449;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 145446 for detecting SNP TSC0036625.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB0000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
DR      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 145446; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 13 BP; 6 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      249 CTCTACCGAAAAA 261
DB      1 CTCTACCGAAAAA 13

RESULT 215
ABF51968/c
ID      ABF51968 standard; DNA; 13 BP.
XX
AC      ABF51968;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 151965 for detecting SNP TSC0038398.
XX

```

CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences									
CC	Sequence	13 BP;	8 A;	3 C;	0 G;	2 T;	0 U;	0 Other;		
XX	Query Match	0.8%; Score 13; DB 1; Length 13;								
XX	Best Local Similarity	100.0%; Pred. No. 95;								
XX	Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1415	CAACTTCAAAAAA	1427							
DB	1	CAACTTCAAAAAA	13							
RESULT 218										
AAT14275/C										
ID	AAT14275	standard; DNA; 14 BP.								
XX	AC	AAT14275;								
XX	DT	29-MAY-1996 (first entry)								
XX	IL-4	and/or IL-13 activated STAT protein binding oligonucleotide.								
XX	Promoter;	heterologous gene; transcriptional regulatory protein; IL-4;								
XX	IL-13;	STAT protein; transcriptional modulation; ss.								
XX	Synthetic.									
XX	WO9528482-A2.									
XX	26-OCT-1995.									
XX	10-APR-1995;	95WO-US004477.								
XX	14-APR-1994;	94US-00228935.								
XX	27-MAR-1995;	95US-00410780.								
XX	(LIGA-)	LIGAND PHARM INC.								
XX	Seidel HM,	Lamb IP;								
XX	WPI;	1995-373797/48.								
XX	DNA spacer	regulatory elements responsive to cytokine(s) - for detecting the presence of transcriptional regulatory protein in a sample.								
XX	Claim 40;	Page 131; 135pp; English.								
XX	The present	oligonucleotide when operably linked to a promoter, and a heterologous gene (HG) selectively binds to an activated transcriptional regulatory protein, comprising a IL-4 and/or IL-13 activated STAT protein, and transcriptionally modulates the HG								
XX	Sequence	14 BP;	2 A;	2 C;	5 G;	5 T;	0 U;	0 Other;		
QY	721	ACTTCCCAGGAAC	733							
DB	14	ACTTCCCAGGAAC	2							
XX	Query Match	0.8%; Score 13; DB 1; Length 14;								
XX	Best Local Similarity	100.0%; Pred. No. 1.1e+02;								
XX	Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0

```
RESULT 219
AAT14274
ID  AAT14274 standard; DNA; 14 BP.
XX
AC  AAT14274;
XX
DT  29-MAY-1996 (first entry)
XX
DE  IL-4 and/or IL-13 activated STAT protein binding oligonucleotide.
XX
KW  Promoter; heterologous gene; transcriptional regulatory protein; IL-4;
KW  IL-13; STAT protein; transcriptional modulation; ss.
XX
OS  Synthetic.
XX
PN  WO9528482-A2.
XX
PD  26-OCT-1995.
XX
PF  10-APR-1995; 95WO-US004477.
XX
PR  14-APR-1994; 94US-00228935.
PR  27-MAR-1995; 95US-00410780.
XX
PA  (LIGA-) LIGAND PHARM INC.
XX
PI  Seidel HM, Lamb IP;
XX
DR  WPI; 1995-373797/48.
XX
DNA spacer regulatory elements responsive to cytokine(s) - for detecting
PT  the presence of transcriptional regulatory protein in a sample.
XX
PS  Claim 40; Page 131; 135pp; English.
XX
CC  The present oligonucleotide when operably linked to a promoter, and a
CC  heterologous gene (HG) selectively binds to an activated transcriptional
CC  regulatory protein, comprising a IL-4 and/or IL-13 activated STAT
CC  protein, and transcriptionally modulates the HG
XX
SQ  Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match      0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  721 ACTTCCCAGGAAC 733
Db  1 ACTTCCCAGGAAC 13

RESULT 220
AAT41588
ID  AAT41588 standard; DNA; 14 BP.
XX
AC  AAT41588;
XX
DT  04-JUN-1997 (first entry)
XX
DE  Cytokine activated STAT6 protein dependent DNA regulatory element.
XX
KW  Regulatory element; STAT6; protein; cytokine; responsive; host cell;
KW  transfection; agonist; antagonist; mediated; transcription; modulation;
KW  signalling pathway; ss.
XX
OS  Synthetic.
XX
PN  WO9630515-A1.
XX
PD  03-OCT-1996.
XX
```

```
PF  25-MAR-1996; 96WO-US004012.
XX
PR  27-MAR-1995; 95US-00411020.
XX
PA  (LIGA-) LIGAND PHARM INC.
XX
PI  Seidel HM, Lamb IP, Tian Chan S;
XX
DR  WPI; 1996-455362/45.
XX
DNA construct for screening modulators of cytokine-mediated transcription
PT  - contg. regulatory element and a cytokine-sensitive promoter operably
PT  linked to a heterologous gene.
XX
PS  Claim 15; Page 63; 72pp; English.
XX
CC  A novel DNA construct comprises an oligonucleotide (ON) comprising a
CC  regulatory element having the present sequence, operably linked to a
CC  promoter, which is operably linked to a heterologous gene (preferably a
CC  marker gene). The gene is under the transcriptional control of the
CC  promoter and the ON sequence when the ON is bound by a STAT6 protein
CC  activated in response to IL-2, IL-3, G-CSF, GM-CSF, erythropoietin,
CC  thrombopoietin, or preferably IL-4, IL-7, IL-9, IL-13 or IL-15. Cytokine
CC  responsive host cells transfected with the DNA construct can be used to
CC  measure the ability of a compound to act as an agonist or antagonist of
CC  cytokine mediated gene transcription. In particular, they can be used to
CC  screen for cytokine modulators involved in the STAT6 protein signalling
CC  pathway
XX
SQ  Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match      0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  721 ACTTCCCAGGAAC 733
Db  1 ACTTCCCAGGAAC 13

RESULT 221
AAV61625
ID  AAV61625 standard; DNA; 14 BP.
XX
AC  AAV61625;
XX
DT  02-DEC-1998 (first entry)
XX
DE  Regulatory element containing oligonucleotide #160.
XX
KW  Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW  transcriptional control; STAT protein; screening; agonist; ss.
XX
OS  Synthetic.
XX
PN  US5814517-A.
XX
PD  29-SEP-1998.
XX
PF  27-MAR-1995; 95US-00410779.
XX
PR  14-APR-1994; 94US-00228935.
XX
PA  (LIGA-) LIGAND PHARM INC.
XX
PI  Lamb IP, Seidel HM;
XX
DR  WPI; 1998-541763/46.
XX
DNA constructs containing cytokine-responsive regulatory elements -
PT  useful in assays for transcription-regulating proteins or gene
PT  transcription agonists or antagonists.
XX
```

PS Example 3; Col 33-34; 58pp; English.

XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the

CC production of constructs comprising a cytokine-responsive regulatory

CC element linked to a promoter which is linked to a heterologous coding

CC sequence so that the coding sequence is under the transcriptional control

CC of the regulatory element and the promoter, where the regulatory element

CC has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA

CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to

CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,

CC in a sample by contacting the sample with the construct so that the

CC protein binds to the regulatory element, and detecting or separating the

CC resulting complex. The cells can be used in screening assays for agonists

CC of gene transcription, in which the level of expression of the coding

CC sequence is measured in the presence and absence of a test compound or in

CC the presence of the corresponding cytokine

XX

SQ Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCCAGGAAC 733

Db 1 ACTTCCCAGGAAC 13

RESULT 222

AAV61626/C

ID AAV61626 standard; DNA; 14 BP.

XX

AC AAV61626;

XX

DT 02-DEC-1998 (first entry)

DE Regulatory element containing oligonucleotide #161.

XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;

KW transcriptional control; STAT protein; screening; agonist; ss.

XX

OS Synthetic.

XX US5814517-A.

PN

XX

PD 29-SEP-1998.

XX

PF 27-MAR-1995; 95US-00410779.

XX

PR 14-APR-1994; 94US-00228935.

XX

PA (LIGA-) LIGAND PHARM INC.

XX

PI Lamb IP, Seidel HM;

XX

DR WPI; 1998-541763/46.

XX

PT DNA constructs containing cytokine-responsive regulatory elements -

PT useful in assays for transcription-regulating proteins or gene

PT transcription agonists or antagonists.

XX

PS Example 3; Col 33-34; 58pp; English.

XX

CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the

CC production of constructs comprising a cytokine-responsive regulatory

CC element linked to a promoter which is linked to a heterologous coding

CC sequence so that the coding sequence is under the transcriptional control

CC of the regulatory element and the promoter, where the regulatory element

CC has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA

CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to

CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,

CC in a sample by contacting the sample with the construct so that the

CC protein binds to the regulatory element, and detecting or separating the

CC

CC resulting complex. The cells can be used in screening assays for agonists

CC of gene transcription, in which the level of expression of the coding

CC sequence is measured in the presence and absence of a test compound or in

CC the presence of the corresponding cytokine

XX

SQ Sequence 14 BP; 2 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCCAGGAAC 733

Db 14 ACTTCCCAGGAAC 2

RESULT 223

AAQ51221

ID AAQ51221 standard; DNA; 15 BP.

XX

AC AAQ51221;

XX

DT 25-MAR-2003 (revised)

DT 12-APR-1994 (first entry)

XX

DE Vaccinia regulatory element sequence.

XX

KW Inhibition; viral replication; infection; ss.

XX

OS Synthetic.

XX WO9320694-A1.

PN

XX

PD 28-OCT-1993.

XX

PF 14-APR-1993; 93WO-US003567.

XX

PR 14-APR-1992; 92US-00868539.

XX

PA (SIGN-) SIGNAL PHARM INC.

XX

PI Carman MD;

XX

DR WPI; 1993-351240/44.

XX

PT Viral replication inhibition in infected cell for e.g. herpes simplex

PT virus-1 - by selecting deoxyribonucleic acid fragment contg. covalently

PT linked strands with sequence corresp. to regulatory element in virus; and

PT introducing in cell.

XX

PS Disclosure; Fig 4; 28pp; English.

XX

CC The viral regulatory sequence from Vaccinia may be introduced into cells

CC to inhibit replication of the virus in the cell and to inhibit viral

CC infection. See also AAQ51213-20. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX

SQ Sequence 15 BP; 9 A; 1 C; 1 G; 3 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.2e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 257 AAAAATGGAATCTA 271

Db 1 AAAAATGGAAYCTA 15

RESULT 224

AAT55111

ID AAT55111 standard; RNA; 15 BP.

XX

AC AAT55111;

XX 25-MAR-2003 (revised)

DT 21-APR-1997 (first entry)

XX Human relA hammerhead ribozyme target sequence (nt. position 996).

DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;

KW Philadelphia chromosome; inflammation; autoimmune disease;

KW atherosclerosis; myocardial infarction; stroke; restenosis;

KW transplant rejection; rheumatoid arthritis; psoriasis;

KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;

KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;

KW ss.

XX Homo sapiens.

OS WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.

PR 29-MAR-1994; 94US-00218934.

PR 04-APR-1994; 94US-00222795.

PR 07-APR-1994; 94US-00224483.

PR 15-APR-1994; 94US-00227958.

PR 15-APR-1994; 94US-00228041.

PR 18-MAY-1994; 94US-00245736.

PR 06-JUL-1994; 94US-00271280.

PR 15-AUG-1994; 94US-00291932.

PR 16-AUG-1994; 94US-00291433.

PR 17-AUG-1994; 94US-00292620.

PR 19-AUG-1994; 94US-00293520.

PR 02-SEP-1994; 94US-00300000.

PR 08-SEP-1994; 94US-00303039.

PR 23-SEP-1994; 94US-00311486.

PR 23-SEP-1994; 94US-00311749.

PR 28-SEP-1994; 94US-00314397.

PR 03-OCT-1994; 94US-00316771.

PR 07-OCT-1994; 94US-00319492.

PR 11-OCT-1994; 94US-00321993.

PR 04-NOV-1994; 94US-00334847.

PR 10-NOV-1994; 94US-00337608.

PR 28-NOV-1994; 94US-00345516.

PR 16-DEC-1994; 94US-00357577.

PR 23-DEC-1994; 94US-00363233.

PR 30-JAN-1995; 95US-00380734.

XX (RIBO-) RIBOZYME PHARM INC.

PA Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;

XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;

PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;

PI Tracz D, Usman N, Wincott FE, Woolf T;

XX WPI; 1995-351090/45.

DR Ribozymes having modified bases and methods for producing them - for use

XX in inhibiting disease related genes.

PT Claim 2; Page 229; 407pp; English.

XX The present sequence represents a preferred target sequence for an

CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the

CC nucleotide base position indicated in the DE line. The relA gene product

CC is a subunit of the transcriptional regulator NF-kappaB and is implicated

CC specifically in the induction of inflammatory responses. Regions of the

CC mRNA that do not form secondary folding structures and that contain

CC potential hammerhead and hairpin ribozyme cleavage sites were identified

CC by computer analysis. Ribozymes directed against these mRNA sequences

CC were designed and synthesised with modifications that improve their

CC nuclease resistance. The ribozymes are designed to cleave the target

CC sequences and thereby inhibit relA expression, making them potentially

CC useful for treating rheumatoid arthritis, restenosis and asthma as well

CC as for increasing tolerance to transplanted tissues. The potential

CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means

CC that uses are limited to local delivery, acute indications or ex vivo

CC treatment. (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 15 BP; 6 A; 3 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 1.2e+02;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1045 GGACATATGAGAC 1057

Db |||||:|||||

2 GGACAUUGAGAC 14

RESULT 225

AAT49860

ID AAT49860 standard; RNA; 15 BP.

XX AAT49860;

AC

XX 07-MAR-1997 (first entry)

DT Human CERP HH ribozyme target sequence #1542.

DE

XX

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;

KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;

KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;

KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;

KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;

KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;

KW LDL; ss.

XX

OS Homo sapiens.

XX WO9620279-A1.

PN

XX

PD 04-JUL-1996.

XX

PF 11-DEC-1995; 95WO-US016000.

XX

PR 23-DEC-1994; 94US-00363240.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (WARN) WARNER LAMBERT CO.

XX

PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;

XX WPI; 1996-321852/32.

DR

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -

PT useful for preventing or treating initial development, progression or

PT regression of vascular diseases, esp. familial hypercholesterolaemia.

XX

PS Claim 4; Page 33; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol

CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-

CC T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid

CC transfer between plasma lipoproteins. The numbering of the targets refers

CC to the position of the cleavage site in full length CERP. The ribozyme

CC binds to 5 nucleotides either side of this site, provided the sequence UH

CC is immediately upstream. The ribozymes are able to cleave mRNA from the

CC gene encoding CERP, thereby blocking synthesis and/or expression of the

CC mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway

CC can be inhibited (or eliminated) thereby preventing the reduction in size

CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypocalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 1 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1577 TGGCTTCCTGCTG 1589
:||||:||||:
Db 3 UGGCUUCUGCUG 15

RESULT 226
AAT49861
ID AAT49861 standard; RNA; 15 BP.
XX
AC AAT49861
XX
DT 07-MAR-1997 (first entry)
XX
DE Human CETP HH ribozyme target sequence #1543.

KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypocalphalipoproteinaemia;
KW peripheral hypercholesterolaemia; dyslipidaemia; hypocalphalipoproteinaemia;
KW angioplastic restenosis; hyperbetalipoproteinaemia; RCT; inhibitor;
KW LDL; ss.

XX Homo sapiens
OS
XX WO9620279-A1.
PN
XX 04-JUL-1996.
PD
XX
PF 11-DEC-1995; 95WO-US016000.
XX
PR 23-DEC-1994; 94US-00363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.

XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
PI
XX WPI; 1996-321852/32.
DR
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
PS Claim 4; Page 33; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence UH
CC is immediately upstream. The ribozymes are able to cleave mRNA from the

CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypocalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 1 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1577 TGGCTTCCTGCTG 1589
:||||:||||:
Db 2 UGGCUUCUGCUG 14

RESULT 227
AAV28329/c
ID AAV28329 standard; DNA; 15 BP.
XX
AC AAV28329;

XX 12-OCT-1998 (first entry)
DT
XX DNA EDTA probe (7) fragment.
DE
XX ss; probe; EDTA probe; specific sequence recognition;
KW chemotherapeutic agent; homopyrimidine-homopurine tract.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT modified_base 22
FT /*tag= a
FT /note= "EDTA thymidine"
XX
PN US5789155-A.
XX
PD 04-AUG-1998.
XX
PF 12-NOV-1993; 93US-00152250.
XX
PR 30-OCT-1987; 87US-00115922.
PR 16-NOV-1990; 90US-00614205.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Moser HE, Dervan PB;
PI
XX WPI; 1998-446067/38.
DR
XX Detection of double-stranded nucleic acid sequence - with triplex-forming
PT oligonucleotide probe.
PT
XX

PS Example 2; Fig 4B; 18pp; English.
XX
XX The EDTA probes 1-9 shown in sequences AAV28326-V28330 contain a single
CC thymidine with EDTA covalently attached at C-5. The probes are used for
CC specific recognition and cleavage of double-stranded DNA or RNA at a
CC sequence specific loci using a triple helix intermediary. The method
CC allows the delivery of chemotherapeutic agents in vivo an eliminates the

CC need to denature the DNA before the agent can act. The method allows
CC precise location of a chemotherapeutic agent or replacement gene sequence
CC at a specific homopyrimidine-homopurine tract anywhere in a large double-
CC stranded nucleic acid. This method allows diagnosis of gene based
CC diseases, and eliminates the need for many steps in the commonly used
CC diagnostic processes
XX
SQ Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1453 AAAAAGAGAAAGA 1465
DB 15 AAAAAGAGAAAGA 3
RESULT 228
AAV48734/C
ID AAV48734 standard; DNA; 15 BP.
XX
AC AAV48734;
XX 15-OCT-1998 (first entry)
XX ErbB-2 gene antisense oligonucleotide ErbB-2-26.
DE ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
KW Synthetic.
XX Homo sapiens.
OS EP856579-A1.
XX 05-AUG-1998.
XX 31-JAN-1997; 97EP-00101531.
PF 31-JAN-1997; 97EP-00101531.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Brysch W;
PI WPI; 1998-400910/35.
DR Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.
XX Claim 10; Fig 6a; 286pp; English.
PS AAV48709-886 represent antisense oligonucleotides directed against the
XX ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in
CC significant reduction in ErbB-2 protein expression, while
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in cases

CC of cancer or (targeting TGF) for stimulating the immune system
XX Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAAGAGGAGG 1389
DB 13 TCTGAAGAGGAGG 1
RESULT 229
AAV31318
ID AAV31318 standard; DNA; 15 BP.
XX
AC AAV31318;
XX 21-MAY-1999 (first entry)
DT Tag sequence of a transcript decreased in colorectal cancer.
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
DE diagnosis; prognosis; treatment; ss.
KW Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998; 98WO-US010277.
PF 21-MAY-1997; 97US-0047352P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
PI WPI; 1999-070161/06.
DR Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX Claim 1; Page 43; 120pp; English.
PS AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
CC in both. The tag sequences can be used to identify genes by matching the
CC tag to a gen data base member, or by using the tag sequences as probes to
CC isolate unidentified genes from cDNA libraries. The tag sequences can
CC also be used in a method for diagnosing colon or pancreatic cancer in a
CC sample suspected of being neoplastic. The method comprises comparing the
CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.
CC The transcript is identified by a tag selected from AAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer
XX Sequence 15 BP; 1 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 513 TGGGCTGGGGGCC 525
DB 3 TGGGCTGGGGGCC 15

RESULT 230
AAF53138
ID AAF53138 standard; DNA; 15 BP.
XX
AC AAF53138;
XX
DT 30-MAR-2001 (first entry)
DE IGF-I oligonucleotide #4098.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 87; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 5 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1397 GGGCCGCAAGAAC 1409
Db 1 GGGCCGCAAGAAC 13
RESULT 231
AAF48239/c
ID AAF48239 standard; DNA; 15 BP.
XX

AC AAF48239;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1659.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 55; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1378 CTGAAGAGGAGGG 1390
Db 15 CTGAAGAGGAGGG 3
RESULT 232
AAF48240/c
ID AAF48240 standard; DNA; 15 BP.
XX
AC AAF48240;
XX
DT 30-MAR-2001 (first entry)
XX

DE IGFBP3 oligonucleotide #1660.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX Homo sapiens.

OS WO200078341-A1.

PN 28-DEC-2000.

PD 21-JUN-2000; 2000WO-AU000693.

PF 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

PI Ameliorating the effects of a disorder, e.g. psoriasis, by administering

XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX Example 7; Page 55; 201pp; English.

PS The present invention relates to a method for ameliorating the effects of

XX skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGAGAGGAGGG 1390

Db 14 CTGAGAGGAGGG 2

RESULT 233

ABK95779

ID ABK95779 standard; DNA; 15 BP.

XX

AC ABK95779;

XX

DT 24-SEP-2002 (first entry)

XX

DE Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #19.

XX

KW Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;

KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;

KW amino acid transporter disorder; single nucleotide polymorphism; SNP.

XX Homo sapiens.

OS WO200244198-A2.

PN 06-JUN-2002.

PD 29-NOV-2001; 2001WO-US044781.

PF 30-NOV-2000; 2000US-0250254P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bieglecki KM, Kazemi A, Russo DP, Sausker EA;

PI WPI; 2002-519580/55.

DR Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral

XX Amino Acid Transporter), Member 4 isogenes, for improving efficiency and

PT reliability in drug development for treating cancers.

PT

XX Claim 15; Page 15; 139pp; English.

PS The invention relates to an isolated polynucleotide (I) comprising a

XX first nucleotide sequence which comprises solute carrier family 1

CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence

CC which is a polymorphic variant of a reference sequence for SLC1A4

CC protein. Also described are methods for: (1) haplotyping or genotyping

CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4

CC gene of an individual; (3) identifying an association between a trait and

CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful

CC in screening for drugs targeting (III) that are useful for treating

CC cancer, neurological diseases and amino acid transporter disorders. The

CC methods are useful for improving the efficiency and reliability of

CC several steps in the discovery and development of drugs for treating

CC diseases associated with SLC1A4 activity. The haplotyping method is also

CC used by the pharmaceutical research scientist to validate SLC1A4 as a

CC candidate target for treating a specific condition or disease predicted

CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases

CC and amino acid transporter disorders, and in the design of clinical

CC trials for treating a specific condition of disease associated with

CC SLC1A4 activity. The methods are also useful for screening compounds

CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic, SLC1A4

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4

CC gene allele-specific oligonucleotides, primer extension oligonucleotides

CC and related PCR primers used to identify single nucleotide polymorphisms

CC (SNP) of the gene

XX

SQ Sequence 15 BP; 2 A; 5 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.2e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 522 GGCTGCACCATGCA 536

Db 1 GGCTGGRCCATGCA 15

RESULT 234

ABQ88675/c

ID ABQ88675 standard; DNA; 15 BP.

XX

AC ABQ88675;

XX

DT 23-SEP-2002 (first entry)

XX

DE Human CFL1 ASO PCR primer #22.

XX

KW Human; cofilin 1; CFL1; gene therapy; antisense gene therapy; primer;

KW immunological disorder; ASO; allele-specific oligonucleotide; PCR; ss.

XX Homo sapiens.
OS
XX WO200194376-A1.
PN
XX
XX
PD 13-DEC-2001.
XX
XX 11-JUN-2001; 2001WO-US018815.
PF
XX
XX 09-JUN-2000; 2000US-0210884P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Anastasio AE, Duda A, Klien SE, Koshy B, Sausker EA;
PI
XX WPI; 2002-566437/60.
DR
XX Novel genetic variants of human cofilin 1, CFL1 gene for studying
PT expression, function of the gene and expressing CFL1 protein useful in
PT identifying drugs to treat immunological disorders.
XX
XX Claim 17; Page 13; 84pp; English.
PS
XX The invention relates to a novel polynucleotide sequence which is a
XX polymorphic variant of a reference sequence for the cofilin 1 (non-
CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
CC the invention may have a use in gene therapy, and in antisense gene
CC therapy. The polynucleotide is useful for studying the expression and
CC function of CFL1 and expressing CFL1 protein for use in screening for
CC candidate drugs to treat diseases related to CFL1 activity. The
CC polymorphism and haplotype data are useful for validating whether CFL1 is
CC a suitable target for drugs to treat immunological disorders, screening
CC for such drugs and reducing bias in clinical trials of such drugs. The
CC present sequence represents one of a set of allele-specific
CC oligonucleotide (ASO) PCR primer used in the invention to detect
CC polymorphisms in the CFL1 gene
XX
SQ Sequence 15 BP; 5 A; 6 C; 2 G; 1 T; 0 U; 1 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.2e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 994 TGCTGATGCTGGGAG 1008
Db 15 TRCTGTTGCTGGGAG 1
RESULT 235
ABT05320/c
ID ABT05320 standard; DNA; 15 BP.
XX
AC ABT05320;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human N-acetylgalactosaminidase (NAGA) alpha gene ASO primer 12.
XX
KW Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
KW chromosome 22q13.2-q13.31; lysosomal glycohydrolase; screening; SNP;
KW NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
KW genotyping.
XX
OS Homo sapiens.
XX
XX WO200194637-A1.
EN
XX
PD 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018456.
PF
XX
XX 07-JUN-2000; 2000US-0210110P.
PR

XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Duda A, Kazemi A, Koshy B, Parks KE;
PI
XX WPI; 2002-566449/60.
XX
XX New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
PT gene, useful for therapeutic purposes, for studying the expression and
PT function of the polynucleotide, and for expressing NAGA protein.
XX
XX Claim 16; Page 13; 91pp; English.
PS
XX The invention comprises the amino acid and coding sequence of the human N
CC -acetylgalactosaminidase (NAGA) alpha protein. The invention specifically
CC comprises novel polymorphic sites identified within the NAGA gene. The
CC NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a
CC lysosomal glycohydrolase that cleaves alpha-N-acetylgalactosaminyl
CC moieties in glycoconjugates. The NAGA DNA and protein sequences of the
CC invention are useful for studying the expression and function of NAGA and
CC for screening candidate drugs to treat diseases related to NAGA activity.
CC The NAGA gene polymorphisms identified in the present invention are
CC useful for haplotyping and genotyping the NAGA gene of an individual. The
CC present DNA sequence represents an N-acetylgalactosaminidase gene allele-
CC specific oligonucleotide primer
XX
SQ Sequence 15 BP; 4 A; 2 C; 3 G; 5 T; 0 U; 1 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.2e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 633 ATTGATATTACCAT 647
Db 15 AYTGATAGTCACCAT 1
RESULT 236
ABQ83689/c
ID ABQ83689 standard; DNA; 15 BP.
XX
AC ABQ83689;
XX
DT 27-JAN-2003 (first entry)
XX
DE DNA-templated synthesis related oligonucleotide #48.
XX
KW Molecular function; diversification; selection; amplification; evolve;
KW synthesis; library; chemical compound; hybridisation; ss.
XX
OS Synthetic.
XX
PN WO200274929-A2.
XX
PD 26-SEP-2002.
XX
PF 19-MAR-2002; 2002WO-US008546.
XX
PR 19-MAR-2001; 2001US-0277081P.
PR 19-MAR-2001; 2001US-0277094P.
PR 20-JUL-2001; 2001US-0306691P.
PR 19-MAR-2002; 2002US-00101030.
XX
XX (HARD) HARVARD COLLEGE.
PA
XX Liu DR, Gartner ZJ, Kanan MW;
PI
XX WPI; 2002-740858/80.
XX
XX Synthesizing chemical compounds by hybridizing one or more templates
PT which have associated reactive unit, with one or more transfer units
PT having anti-codon and reactive unit, and performing reaction of reactive
PT units.

XX Example 7; Fig 44; 146pp; English.

PS The present invention describes a method (M1) for synthesising one or

XX more chemical compounds. M1 involves providing one or more templates,

CC which optionally have a reactive unit associated with them; and

CC contacting one or more transfer units having an anti-codon and reactive

CC unit with the one or more templates under conditions to allow for

CC hybridisation of the one or more anti-codons to template, and reaction of

CC the reactive units. Also described: (1) a method (M2) of evolving a

CC library of compounds; (2) a kit comprising one or more nucleic acid

CC templates and one or more transfer units; (3) a method (M3) for

CC synthesising one or more non-natural polymers; and (4) a library (I)

CC comprising one or more chemical compounds where each of the chemical

CC compounds is bonded to an amplifiable template whose nucleotide sequence

CC is informative of the structure of the chemical compounds, where the

CC library is synthesised by M1 or M3. The method can be used for

CC synthesising one or more chemical compounds which contain an anti-codon

CC comprising a nucleotide sequence which hybridises with one or more

CC nucleic acid templates. M1 is useful for synthesising a library of

CC chemical compounds. The methods are useful for synthesising chemical

CC compounds that are not, or do not resemble nucleic acids or nucleic acid

CC analogues. The present sequence represents an oligonucleotide which is

XX used in an example from the present invention

SQ Sequence 15 BP; 4 A; 6 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CGCTGGTGTGCTGCT 31

DB 15 CGCTGGTGTGCTGCT 3

RESULT 237

ABK96592

ID ABK96592 standard; DNA; 15 BP.

XX

AC ABK96592;

XX

DT 24-SEP-2002 (first entry)

XX

DE Human interleukin 6 allele specific primer #15.

XX

KW Human; ss; primer; interleukin-6; IL6; myeloma; arthritis; CAD;

KW Kaposi sarcoma; coronary artery disease; inflammatory cytokine;

KW hypercalcaemia; bone disease; inflammatory disease; HIV; PCR;

KW human immunodeficiency virus infection; stunted growth; isogene;

KW systemic onset juvenile chronic arthritis; haplotype; genotype;

KW chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO200238586-A2.

XX

PD 16-MAY-2002.

XX

PF 09-NOV-2001; 2001WO-US047077.

XX

PR 09-NOV-2000; 2000US-0247578P.

PR 21-AUG-2001; 2001US-0313963P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M;

PI Nandabalan K, Parks KE, Sausker EA;

XX

DR WPI; 2002-519290/55.

XX

PT Genetic variants of interleukin-6 isogenes for improving efficiency and

PT reliability in drug development for treating myeloma, coronary artery

PT disease, arthritis and Kaposi sarcoma.

XX

PS Claim 15; Page 15; 86pp; English.

XX

CC The invention relates to a polynucleotide comprising a first nucleotide

CC sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine)

CC isogene selected from isogenes 1-11 and 13-18 given in the specification,

CC where each isogene comprises the regions of NS1 and is further defined by

CC the corresponding sequence of polymorphisms whose locations and

CC identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17),

CC or a second nucleotide sequence (NS2) complementary to NS1.

CC Alternatively, the sequence comprises a coding sequence for an IL6

CC isogene. Also included are methods of haplotyping/ genotyping (and

CC predicting the haplotype/genotype) of the IL6 gene of an individual,

CC identifying an association between a trait and at least one haplotype or

CC haplotype pair of the IL6 gene, an isolated oligonucleotide for detecting

CC a polymorphism in the IL6 gene, a recombinant non-human organism (III)

CC transformed or transfected with the IL6 polynucleotide, an isolated

CC fragment of the IL6 isogene comprising at least 10 and containing one of

CC the identified single- nucleotide polymorphisms (SNP), an isolated

CC polypeptide (or fragment) comprising an amino acid sequence which is a

CC polymorphic variant of IL6, an isolated monoclonal antibody specific for

CC IL6, a computer system for storing and analysing polymorphism data for

CC the IL6 gene, and a genome anthology for the IL6 gene. The IL6

CC polymorphic variant is useful in screening for drugs targeting IL6 that

CC are useful for treating myeloma, coronary artery disease (CAD),

CC arthritis, Kaposi sarcoma (associated with human immunodeficiency virus

CC infection, HIV), hypercalcaemia, bone disease, inflammatory disease,

CC stunted growth and systemic onset juvenile chronic arthritis. The methods

CC are useful for improving the efficiency and reliability in the discovery

CC and development of drugs and in the validation of IL6 as a drug target.

CC The antibody is useful in diagnostic, prognostic and therapeutic methods.

CC The IL6 isogene is useful in studying the expression and function of IL6,

CC and in expressing IL6 protein for use in screening for candidate drugs.

CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence

CC is an allele specific primer for an IL6 polymorphism

XX

SQ Sequence 15 BP; 5 A; 2 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.2e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1537 AGGAGGAGGCCAAGT 1551

DB 1 ATGAGGAGGCCAAT 15

RESULT 238

ABZ34008/c

ID ABZ34008 standard; DNA; 15 BP.

XX

AC ABZ34008;

XX

DT 31-JAN-2003 (first entry)

XX

DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:250.

XX

KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;

KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;

KW probe; ss.

XX

OS Human immunodeficiency virus 1.

OS Synthetic.

XX

PN WO200255741-A2.

XX

PD 18-JUL-2002.

XX

PF 09-JAN-2002; 2002WO-EP000153.

XX

PR 11-JAN-2001; 2001EP-00870005.

PR 20-APR-2001; 2001EP-00870085.

PR 24-APR-2001; 2001US-0286102P.
 XX (INNO-) INNOGENETICS NV.
 PA De Smet K, Stuyver L;
 XX WPI; 2002-590680/63.
 DR
 XX Detecting mutations associated with anti-HIV drug resistance comprises
 PT detecting at least one of the mutations in the HIV reverse transcriptase
 PT gene by using probes optimized to function together in a reverse-
 PT hybridization assay.
 XX Claim 2; Page 19; 117pp; English.
 PS
 XX The present invention describes a method for detecting mutations
 CC associated with anti-HIV drug resistance in a patient by detecting at
 CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, Y188L,
 CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
 CC of HIV strains in a biological sample using a specific set of probes
 CC optimised to function together in a reverse-hybridisation assay. The
 CC method and the nucleic acid sequences used in the method are useful for
 CC determining viral mutations and/or polymorphisms in the HIV RT gene
 CC associated with resistance. The probes are useful for the genetic
 CC detection, preferably in vitro detection of the mutations K103N/R,
 CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
 CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
 CC mutation is associated with anti-HIV drug resistance. The method provides
 CC a rapid, reliable and precise assay or determination and monitoring of
 CC antiviral drug resistance or mutations associated with drug resistance of
 CC viruses containing RT genes. AB233759 to AB234642 represent HIV RT
 CC sequences and probes which are used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1273 CCATCCCTGAGGA 1285
 DB 15 CCATCCCTGAGGA 3
 RESULT 239
 ABK32272
 ID ABK32272 standard; DNA; 15 BP.
 XX
 AC ABK32272;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human colon cancer SAGE tag #373.
 XX
 KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
 KW serial analysis of gene expression; diagnostic; prognostic; probe;
 KW cancer marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6333152-B1.
 XX
 PD 25-DEC-2001.
 XX
 PF 20-MAY-1998; 98US-00081646.
 XX
 PR 20-MAY-1998; 98US-00081646.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
 XX

DR WPI; 2002-153821/20.
 XX
 PT New human nucleic acid containing specific SAGE tags, useful as
 PT diagnostic markers for cancer, also derived probes.
 XX
 PS Disclosure; Col 42; 161pp; English.
 XX
 CC The invention relates to an isolated, purified human nucleic acid (I)
 CC that has the same sequence as a mRNA found in humans and is a SAGE
 CC (serial analysis of gene expression) tag comprising a single stranded
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
 CC diagnostic and prognostic markers of cancer, especially of the colon and
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
 CC SAGE tags of the invention
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 513 TGGGCTGGGGGCC 525
 DB 3 TGGGCTGGGGGCC 15
 RESULT 240
 ABI99094
 ID ABI99094 standard; DNA; 15 BP.
 XX
 AC ABI99094;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human PCDH2 ASO PCR primer SEQ ID NO 51.
 XX
 KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
 KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
 KW allele-specific oligonucleotide; ASO; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200194361-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 06-JUN-2001; 2001WO-US018321.
 XX
 PR 06-JUN-2000; 2000US-0209564P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Kliem SE, Koshy B, Tanguay DA;
 XX
 DR WPI; 2002-097928/13.
 XX
 PT New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
 PT useful in expressing PCDH2 protein for screening candidate drugs to treat
 PT diseases related to PCDH2 activity.
 XX
 PS Claim 16; Page 14; 127pp; English.
 XX
 CC The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
 CC comprising determining which of the haplotypes given in the specification
 CC defines one or both copies of the individual's PCDH2 gene. The
 CC polymorphisms are within a 3024 base pair sequence (ABA05413), fully
 CC defined in the specification. The polymorphic variants are useful in
 CC studying the expression and function of PCDH2, in expressing PCDH2
 CC protein for use in screening for candidate drugs to treat diseases such
 CC as cancer, related to PCDH2 activity, in studying the effect of the
 CC variation on the biological activity of PCDH2 and the binding affinity of
 CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
 CC validating PCDH2 as a candidate target for treating a specific condition
 CC

XX 25-OCT-2001.
PD
XX
XX
PF 13-APR-2001; 2001WO-US012245.
XX
XX
PR 13-APR-2000; 2000US-00548797.
XX
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX
PI Keith T;
XX
DR WPI; 2001-639428/73.
XX
XX
XX Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
PT proteins they encode, useful for the prevention, diagnosis and treatment
PT of asthma, obesity and inflammatory bowel disease.
XX
XX
PS Example 11; Page 156; 520pp; English.
XX
XX
CC The invention relates to isolated genes (Gene 216) from human chromosome
CC 20p13-p12 and the proteins they encode. The nucleic acids and proteins
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate Gene 216 expression. For example, the
CC nucleic acids (or vectors) and proteins may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of gene 216 by expressing
CC inactive proteins or to supplement the patient's own production of Gene
CC 216 proteins. Additionally, the nucleic acids may be used to produce the
CC secreted Gene 216 protein, by inserting the nucleic acids into a host
CC cell and culturing the cell to express the protein. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acid
CC sequences in samples and therefore which patients may be in need of
CC restorative therapy. The Gene 216 protein may also be used as antigens in
CC the production of antibodies against Gene 216 and in assays to identify
CC modulators of Gene 216 expression and activity. The anti-Gene 216
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-Gene 216 antibodies may also be used as diagnostic
CC agents for detecting the presence of Gene 216 proteins in samples (e.g.
CC by enzyme linked immunosorbant assay or ELISA). Disorders that may be
CC prevented, diagnosed and/or treated by the above methods include, for
CC example asthma, obesity and inflammatory bowel disease. The present
CC sequence is that of a Gene 216 related primer used in examples of the
CC invention. The primers are used in the physical mapping of the gene
CC (ABZ72067-ABZ72088), polymorphism identification using single strand
CC conformational polymorphism (SSCP) analysis (ABZ72091-ABZ72184),
CC sequencing (ABZ72185-ABZ72268) and genotyping (ABZ72317-ABZ72362)

XX
SQ Sequence 16 BP; 3 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1
RESULT 244
ABX75211/C
ID ABX75211 standard; DNA; 16 BP.
XX
XX
AC ABX75211;
XX
XX
DT 25-MAR-2003 (first entry)
XX
XX
DE Human 216 gene allele specific oligonucleotide probe #42.
XX
KW Human; mouse; ss; probe; gene 216; antiasthmatic; antiinflammatory;
KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;
KW gene therapy; respiratory disease; asthma; obesity;
KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;

KW adult respiratory distress syndrome; inflammatory bowel syndrome.
XX
OS Homo sapiens.
XX
XX
PN WO200283077-A2.
XX
XX
PD 24-OCT-2002.
XX
XX
PF 15-APR-2002; 2002WO-US012063.
XX
XX
PR 13-APR-2001; 2001US-00834597.
PR 13-APR-2001; 2001WO-US012245.
XX
XX
PA (SCHE) SCHERING CORP.
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX
PI Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Mastro RG;
PI Simon J, Allen K, Pandit S;
XX
DR WPI; 2003-092960/08.
XX
XX
XX New isolated gene 216 nucleic acids, useful for diagnosing, preventing or
PT treating a disorder, such as asthma, bronchial hyper-responsiveness,
PT chronic obstructive pulmonary disease, obesity or inflammatory bowel
PT syndrome.
XX
PS Example 10; Page 167; 650pp; English.
XX
XX
CC This invention relates to a novel isolated nucleic acid, gene 216,
CC identified from human chromosome 20p13-p12. The invention also discloses
CC regions of the 216 gene that contain single nucleotide polymorphisms
CC (SNP's) which may be used as markers for disease susceptibility or
CC severity. The nucleotides of the invention may have antiasthmatic,
CC antiinflammatory or anorectic activities and may be used in gene therapy.
CC The nucleic acids, antibodies or its fragments are useful for diagnosing,
CC preventing or treating a disorder, such as respiratory diseases (e.g.
CC asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary
CC disease or adult respiratory distress syndrome), obesity, or inflammatory
CC bowel syndrome. The nucleic acids are also useful for identifying
CC increased susceptibility of a subject to the disorders mentioned. The
CC nucleic acids can also be used as primers and templates for the
CC recombinant production of disorder-associated peptides or polypeptides,
CC for chromosome and gene mapping, or for tissue distribution studies. The
CC present sequence represents a gene 216 specific oligonucleotide probe
XX used in the scope of the invention
SQ Sequence 16 BP; 3 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1
Search completed: June 24, 2004, 10:08:26
Job time : 6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 09:51:10 ; Search time 7 Seconds
(without alignments)
1.692 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgcccg.....tcctcagctttttttcccc 1611

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 194 seqs, 3677 residues

Total number of hits satisfying chosen parameters: 388

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 194 summaries

Database : rge2.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	26	1.6	26	1 BD244917	ACCESSION:BD244917
C 2	26	1.6	26	1 AX053080	ACCESSION:AX053080
C 3	26	1.6	26	1 AX053089	ACCESSION:AX053089
C 4	26	1.6	26	1 AX546298	ACCESSION:AX546298
C 5	26	1.6	26	1 AX546388	ACCESSION:AX546388
C 6	25	1.6	26	1 AX546341	ACCESSION:AX546341
C 7	25	1.6	26	1 AX546431	ACCESSION:AX546431
C 8	24.4	1.5	26	1 AX053078	ACCESSION:AX053078
C 9	24.4	1.5	26	1 AX053079	ACCESSION:AX053079
C 10	24.4	1.5	26	1 AX053087	ACCESSION:AX053087
C 11	24.4	1.5	26	1 AX053088	ACCESSION:AX053088
C 12	23.4	1.5	26	1 AX546333	ACCESSION:AX546333
C 13	23.4	1.5	26	1 AX546334	ACCESSION:AX546334
C 14	23.4	1.5	26	1 AX546423	ACCESSION:AX546423
C 15	23.4	1.5	26	1 AX546424	ACCESSION:AX546424
C 16	23	1.4	23	1 BD244915	ACCESSION:BD244915
C 17	23	1.4	23	1 AX546296	ACCESSION:AX546296
C 18	23	1.4	23	1 AX546386	ACCESSION:AX546386
C 19	22.8	1.4	26	1 BD244923	ACCESSION:BD244923
C 20	22.8	1.4	26	1 AX053081	ACCESSION:AX053081
C 21	22.8	1.4	26	1 AX053090	ACCESSION:AX053090
C 22	22.8	1.4	26	1 AX546306	ACCESSION:AX546306
C 23	22.8	1.4	26	1 AX546396	ACCESSION:AX546396
C 24	22	1.4	22	1 BD244916	ACCESSION:BD244916
C 25	22	1.4	22	1 AX546297	ACCESSION:AX546297
C 26	22	1.4	22	1 AX546387	ACCESSION:AX546387
C 27	21.8	1.4	26	1 AX546340	ACCESSION:AX546340
C 28	21.8	1.4	26	1 AX546430	ACCESSION:AX546430
C 29	21.4	1.3	23	1 BD244920	ACCESSION:BD244920
C 30	21.4	1.3	23	1 BD244921	ACCESSION:BD244921
C 31	21.4	1.3	23	1 AX546304	ACCESSION:AX546304
C 32	21.4	1.3	23	1 AX546394	ACCESSION:AX546394
C 33	20.4	1.3	22	1 BD244922	ACCESSION:BD244922

C 34	20.4	1.3	22	1 AX546305	ACCESSION:AX546305
C 35	20.4	1.3	22	1 AX546395	ACCESSION:AX546395
C 36	20	1.2	20	1 BD244905	ACCESSION:BD244905
C 37	20	1.2	20	1 BD244906	ACCESSION:BD244906
C 38	20	1.2	20	1 BD244907	ACCESSION:BD244907
C 39	20	1.2	20	1 BD244908	ACCESSION:BD244908
C 40	20	1.2	20	1 BD244909	ACCESSION:BD244909
C 41	20	1.2	20	1 BD244911	ACCESSION:BD244911
C 42	20	1.2	20	1 BD244913	ACCESSION:BD244913
C 43	20	1.2	20	1 BD244914	ACCESSION:BD244914
C 44	20	1.2	20	1 AX053077	ACCESSION:AX053077
C 45	20	1.2	20	1 AX053086	ACCESSION:AX053086
C 46	20	1.2	20	1 AX456071	ACCESSION:AX456071
C 47	20	1.2	20	1 AX456072	ACCESSION:AX456072
C 48	20	1.2	20	1 AX546286	ACCESSION:AX546286
C 49	20	1.2	20	1 AX546287	ACCESSION:AX546287
C 50	20	1.2	20	1 AX546288	ACCESSION:AX546288
C 51	20	1.2	20	1 AX546289	ACCESSION:AX546289
C 52	20	1.2	20	1 AX546290	ACCESSION:AX546290
C 53	20	1.2	20	1 AX546292	ACCESSION:AX546292
C 54	20	1.2	20	1 AX546294	ACCESSION:AX546294
C 55	20	1.2	20	1 AX546295	ACCESSION:AX546295
C 56	20	1.2	20	1 AX546376	ACCESSION:AX546376
C 57	20	1.2	20	1 AX546377	ACCESSION:AX546377
C 58	20	1.2	20	1 AX546378	ACCESSION:AX546378
C 59	20	1.2	20	1 AX546379	ACCESSION:AX546379
C 60	20	1.2	20	1 AX546380	ACCESSION:AX546380
C 61	20	1.2	20	1 AX546382	ACCESSION:AX546382
C 62	20	1.2	20	1 AX546384	ACCESSION:AX546384
C 63	20	1.2	20	1 AX546385	ACCESSION:AX546385
C 64	20	1.2	20	1 AX703613	ACCESSION:AX703613
C 65	20	1.2	20	1 AX703614	ACCESSION:AX703614
C 66	19.2	1.2	24	1 AX173370	ACCESSION:AX173370
C 67	18.4	1.1	20	1 BD244912	ACCESSION:BD244912
C 68	18.4	1.1	20	1 AX546291	ACCESSION:AX546291
C 69	18.4	1.1	20	1 AX546293	ACCESSION:AX546293
C 70	18.4	1.1	20	1 AX546381	ACCESSION:AX546381
C 71	18.4	1.1	20	1 AX546383	ACCESSION:AX546383
C 72	17	1.1	17	1 AX733295	ACCESSION:AX733295
C 73	17	1.1	17	1 AX733529	ACCESSION:AX733529
C 74	16.8	1.0	20	1 BD244910	ACCESSION:BD244910
C 75	16.8	1.0	20	1 AX462615	ACCESSION:AX462615
C 76	16.4	1.0	20	1 AR029137	ACCESSION:AR029137
C 77	16.4	1.0	20	1 AR036521	ACCESSION:AR036521
C 78	16.4	1.0	20	1 AR073958	ACCESSION:AR073958
C 79	16.4	1.0	20	1 AR096054	ACCESSION:AR096054
C 80	16.4	1.0	20	1 AR105513	ACCESSION:AR105513
C 81	16.4	1.0	20	1 E49537	ACCESSION:E49537
C 82	16.4	1.0	20	1 I27257	ACCESSION:I27257
C 83	16.4	1.0	20	1 AR212287	ACCESSION:AR212287
C 84	16.4	1.0	20	1 AR215981	ACCESSION:AR215981
C 85	16.4	1.0	20	1 AR231421	ACCESSION:AR231421
C 86	15.4	1.0	17	1 BD255496	ACCESSION:BD255496
C 87	15.4	1.0	17	1 BD255497	ACCESSION:BD255497
C 88	15.4	1.0	18	1 AR293317	ACCESSION:AR293317
C 89	14.8	0.9	18	1 AR035154	ACCESSION:AR035154
C 90	14.8	0.9	18	1 AR127642	ACCESSION:AR127642
C 91	14.8	0.9	18	1 AR174568	ACCESSION:AR174568
C 92	14.8	0.9	18	1 BD237586	ACCESSION:BD237586
C 93	14.8	0.9	18	1 BD237603	ACCESSION:BD237603
C 94	14.8	0.9	18	1 BD248961	ACCESSION:BD248961
C 95	14.8	0.9	18	1 I75311	ACCESSION:I75311
C 96	14.8	0.9	18	1 AR342894	ACCESSION:AR342894
C 97	14.8	0.9	18	1 AR342911	ACCESSION:AR342911
C 98	14.8	0.9	18	1 AR374060	ACCESSION:AR374060
C 99	14.8	0.9	18	1 AJ597665	ACCESSION:AJ597665
C 100	14.4	0.9	16	1 BD231175	ACCESSION:BD231175
C 101	14.4	0.9	16	1 AR242277	ACCESSION:AR242277
C 102	14.4	0.9	16	1 AR328425	ACCESSION:AR328425
C 103	14.4	0.9	16	1 AX503577	ACCESSION:AX503577
C 104	14.4	0.9	17	1 BD255495	ACCESSION:BD255495
C 105	14.4	0.9	17	1 BD255498	ACCESSION:BD255498
C 106	14.4	0.9	17	1 AR327352	ACCESSION:AR327352

C 107	14.4	0.9	17	1	AX217646	ACCESSION:AX217646	C 180	13	0.8	16	1	AX327134	ACCESSION:AX327134
C 108	14.4	0.9	17	1	AX218225	ACCESSION:AX218225	C 181	12.8	0.8	16	1	A18727	ACCESSION:A18727
C 109	14.4	0.9	17	1	AX475558	ACCESSION:AX475558	182	12.8	0.8	16	1	A29549	ACCESSION:A29549
C 110	14.4	0.9	17	1	AX475559	ACCESSION:AX475559	183	12.8	0.8	16	1	A42606	ACCESSION:A42606
C 111	14.4	0.9	17	1	AX784017	ACCESSION:AX784017	184	12.8	0.8	16	1	A88795	ACCESSION:A88795
C 112	14.4	0.9	17	1	AX784018	ACCESSION:AX784018	185	12.8	0.8	16	1	AR073525	ACCESSION:AR073525
C 113	14.4	0.9	18	1	AR267656	ACCESSION:AR267656	186	12.8	0.8	16	1	BD244651	ACCESSION:BD244651
114	14.4	0.9	18	1	AR292367	ACCESSION:AR292367	187	12.8	0.8	16	1	E05495	ACCESSION:E05495
C 115	14.4	0.9	18	1	AR297444	ACCESSION:AR297444	188	12.8	0.8	16	1	AR221701	ACCESSION:AR221701
C 116	14.4	0.9	18	1	BD057516	ACCESSION:BD057516	189	12.8	0.8	16	1	AR254651	ACCESSION:AR254651
C 117	14	0.9	17	1	AX727187	ACCESSION:AX727187	190	12.8	0.8	16	1	AR257446	ACCESSION:AR257446
C 118	14	0.9	17	1	AX784019	ACCESSION:AX784019	191	12.8	0.8	16	1	AR328586	ACCESSION:AR328586
C 119	14	0.9	17	1	AX784020	ACCESSION:AX784020	192	12.8	0.8	16	1	AR343259	ACCESSION:AR343259
C 120	13.8	0.9	17	1	A12195	ACCESSION:A12195	193	12.8	0.8	16	1	AR367752	ACCESSION:AR367752
C 121	13.8	0.9	17	1	A26903	ACCESSION:A26903	194	12.8	0.8	16	1	BD066308	ACCESSION:BD066308

RESULT 1
BD244917/c

BD244917 26 bp DNA linear
 Modulation of gene expression by combination therapy.
 BD244917
 BD244917.1 GI:33054687
 JP 2002528391-A/45.
 synthetic construct
 synthetic construct
 artificial sequences.
 1 (bases 1 to 26)
 Besterman, J.M., Macleod, A.R. and Siders, W.M.
 Modulation of gene expression by combination therapy.
 Patent: JP 2002528391-A 45 03-SEP-2002;
 JOURNAL

```

Query Match          1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 211 GAATCCGCATGACTCATAAATTGCTG 236
|||
db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 2
AX053080/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 4 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1
RESULT 3
LOCUS AX053089 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 13 from Patent WO0071703.
ACCESSION AX053089
VERSION AX053089.1 GI:12227146
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 13 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1
RESULT 4
LOCUS AX546298 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 47 from Patent EP1243290.
ACCESSION AX546298
VERSION AX546298.1 GI:25811489
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 47 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1
RESULT 5
LOCUS AX546388 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 47 from Patent EP1243289.
ACCESSION AX546388
VERSION AX546388.1 GI:25811579
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 47 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1
RESULT 6
LOCUS AX546341 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 90 from Patent EP1243290.
ACCESSION AX546341
VERSION AX546341.1 GI:25811532
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 90 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 AATCCGCATGACTCATAATTGCTG 236

Db 25 AATCCGCATGACTCATAATTGCTG 1
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RESULT 7
AX546431/c
LOCUS AX546431 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 90 from Patent EP1243289.
ACCESSION AX546431
VERSION AX546431.1 GI:25811622
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 90 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 AATCCGCATGACTCATAATTGCTG 236
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Db 25 AATCCGCATGACTCATAATTGCTG 1
|||||
RESULT 8
AX053078/c
LOCUS AX053078 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 2 from Patent WO0071703.
ACCESSION AX053078
VERSION AX053078.1 GI:12227135
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 2 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
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Db 26 GAATCCGCATGACCCATAATTGCTG 1
|||||
RESULT 9
AX053079/c
LOCUS AX053079 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 3 from Patent WO0071703.
ACCESSION AX053079
VERSION AX053079.1 GI:12227136
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 3 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||||
Db 26 GAATCCGCATGACTCATAACTTGCTG 1
|||||
RESULT 10
AX053087/c
LOCUS AX053087 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 11 from Patent WO0071703.
ACCESSION AX053087
VERSION AX053087.1 GI:12227144
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 11 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"
Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
|||||
Db 26 GAATCCGCATGACCCATAATTGCTG 1
|||||
RESULT 11
AX053088/c
LOCUS AX053088 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 12 from Patent WO0071703.
ACCESSION AX053088
VERSION AX053088.1 GI:12227145
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 12 30-NOV-2000;
Methylgene, Inc. (CA)

FEATURES		Location/Qualifiers	
source	1. .26		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
	/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"		
Query Match			
	1.5%;	Score 24.4;	DB 1; Length 26;
Best Local Similarity	96.2%;	Pred. No. 14;	
Matches	25; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	211 GAATCCGCATGACTCATAATTGCTG	236	
Db	26 GAATCCGCATGACTCATAATTGCTG	1	
RESULT 12			
AX546333/c	LOCUS	AX546333	26 bp DNA linear PAT 26-NOV-2002
DEFINITION	Sequence 82 from Patent EP1243290.		
ACCESSION	AX546333		
VERSION	AX546333.1	GI:25811524	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Besterman,J.M., Macleod,A.R. and Siders,W.M.		
TITLE	Modulation of gene expression by combination therapy		
JOURNAL	Patent: EP 1243290-A 82 25-SEP-2002;		
	Methylgene, Inc. (CA)		
FEATURES		Location/Qualifiers	
source	1. .26		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="oligonucleotide"		
Query Match			
	1.5%;	Score 23.4;	DB 1; Length 26;
Best Local Similarity	96.0%;	Pred. No. 19;	
Matches	24; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	212 AATCCGCATGACTCATAATTGCTG	236	
Db	25 AATCCGCATGACCCATAATTGCTG	1	
RESULT 13			
AX546334/c	LOCUS	AX546334	26 bp DNA linear PAT 26-NOV-2002
DEFINITION	Sequence 83 from Patent EP1243290.		
ACCESSION	AX546334		
VERSION	AX546334.1	GI:25811525	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Besterman,J.M., Macleod,A.R. and Siders,W.M.		
TITLE	Modulation of gene expression by combination therapy		
JOURNAL	Patent: EP 1243290-A 83 25-SEP-2002;		
	Methylgene, Inc. (CA)		
FEATURES		Location/Qualifiers	
source	1. .26		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="oligonucleotide"		
Query Match			
	1.5%;	Score 23.4;	DB 1; Length 26;
Best Local Similarity	96.0%;	Pred. No. 19;	


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ACCESSION BD244915
VERSION BD244915.1 GI:33054685
KEYWORDS JP 2002528391-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 43 03-SEP-2002;
METHYLENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/43
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source
FT 1. .23
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source
Location/Qualifiers
1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 17
AX546296/c
LOCUS AX546296 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 45 from Patent EP1243290.
ACCESSION AX546296
VERSION AX546296.1 GI:25811487
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 45 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide"
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 18
AX546386/c
LOCUS AX546386 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 45 from Patent EP1243289.
ACCESSION AX546386
VERSION AX546386.1 GI:25811577
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 45 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1. .23
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide"
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 19
BD244923/c
LOCUS BD244923 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy
ACCESSION BD244923
VERSION BD244923.1 GI:33054693
KEYWORDS JP 2002528391-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 51 03-SEP-2002;
METHYLENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/51
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide"
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATATTGCTG 236

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Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 20
AX053081/c
LOCUS
DEFINITION
Sequence 5 from Patent WO0071703.
ACCESSION
AX053081
VERSION
AX053081.1 GI:12227138
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE
Inhibition of histone deacetylase
JOURNAL
Patent: WO 0071703-A 5 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 21
AX053090/c
LOCUS
DEFINITION
Sequence 14 from Patent WO0071703.
ACCESSION
AX053090
VERSION
AX053090.1 GI:12227147
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE
Inhibition of histone deacetylase
JOURNAL
Patent: WO 0071703-A 14 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 22
AX546306/c
LOCUS
DEFINITION
Sequence 55 from Patent EP1243290.
ACCESSION
AX546306

VERSION
AX546306.1 GI:25811497
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE
Modulation of gene expression by combination therapy
JOURNAL
Patent: EP 1243290-A 55 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 23
AX546396/c
LOCUS
DEFINITION
Sequence 55 from Patent EP1243289.
ACCESSION
AX546396
VERSION
AX546396.1 GI:25811587
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE
Modulation of gene expression by combination therapy
JOURNAL
Patent: EP 1243289-A 55 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGCTG 1
RESULT 24
BD244916/c
LOCUS
DEFINITION
Modulation of gene expression by combination therapy.
ACCESSION
BD244916
VERSION
BD244916.1 GI:33054686
KEYWORDS
JP 2002528391-A/44.
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 22)
AUTHORS
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE
Modulation of gene expression by combination therapy
JOURNAL
Patent: JP 2002528391-A 44 03-SEP-2002;
METHYLGENE INC
COMMENT
OS Artificial Sequence

PN JP 2002528391-A/44
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN, ALAN ROBERT MACLEOD, WILLIAM M SIDERS PC
A61K48/00, A61K31/165, A61K31/19, A61K31/513, A61K31/517, A61K31/ PC
706,
PC
A61K31/7068, A61K31/7088, A61K31/7125, A61K45/00, A61P35/00, C12N15/ PC
09//
PC C12N5/10, C12N15/00, C12N5/00
CC antisense Location/Qualifiers
FH key 1..22
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAAATTACTATTATGGACA 187
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Db 22 TTGGAAATTACTATTATGGACA 1

RESULT 25
AX546297/c
LOCUS AX546297 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 46 from Patent EP1243290.
ACCESSION AX546297
VERSION AX546297.1 GI:25811488
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 46 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAAATTACTATTATGGACA 187
|||||
Db 22 TTGGAAATTACTATTATGGACA 1

RESULT 26
AX546387/c
LOCUS AX546387 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 46 from Patent EP1243289.
ACCESSION AX546387
VERSION AX546387.1 GI:25811578
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.

TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 46 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAAATTACTATTATGGACA 187
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Db 22 TTGGAAATTACTATTATGGACA 1

RESULT 27
AX546340/c
LOCUS AX546340 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 89 from Patent EP1243290.
ACCESSION AX546340
VERSION AX546340.1 GI:25811531
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 89 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.4%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 29;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATTAATTGCTG 236
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Db 25 AATCCGCATGACCCATAACTTGCTG 1

RESULT 28
AX546430/c
LOCUS AX546430 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 89 from Patent EP1243289.
ACCESSION AX546430
VERSION AX546430.1 GI:25811621
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 89 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.4%; Score 21.8; DB 1; Length 26;
Besterman, J.M., Macleod, A.R. and Siders, W.M.

Best Local Similarity 92.0%; Pred. No. 29;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTATAATTGCTG 236
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Db 25 AATCCGCATGACCCATAACTTGCTG 1

RESULT 29
BD244920/c
LOCUS BD244920 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244920
VERSION BD244920.1 GI:33054690
KEYWORDS JP 2002528391-A/48.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 23)
REFERENCE Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: JP 2002528391-A 48 03-SEP-2002;
JOURNAL METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/48
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
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FH Key Location/Qualifiers
FT source 1. .23
/organism='Artificial Sequence'

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
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Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 31
AX546304/c
LOCUS AX546304 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 53 from Patent EP1243290.
ACCESSION AX546304
VERSION AX546304.1 GI:25811495
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: EP 1243290-A 53 25-SEP-2002;
JOURNAL Methylgene, Inc. (CA)
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source 1. .23
/organism='synthetic construct'
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Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
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QY 138 AAAGTCTGTTACTACTACGACGG 160
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Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 32
AX546394/c
LOCUS AX546394 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 53 from Patent EP1243289.
ACCESSION AX546394
VERSION AX546394.1 GI:25811585
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: EP 1243289-A 53 25-SEP-2002;
JOURNAL Methylgene, Inc. (CA)

PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
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PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1. .23
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FEATURES
source 1. .23
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Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
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RESULT 31
AX546304/c
LOCUS AX546304 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 53 from Patent EP1243290.
ACCESSION AX546304
VERSION AX546304.1 GI:25811495
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
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REFERENCE Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: EP 1243290-A 53 25-SEP-2002;
JOURNAL Methylgene, Inc. (CA)
FEATURES
source 1. .23
/organism='synthetic construct'
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/db_xref='taxon:32630'
/note='oligonucleotide'

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
|||||
Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 32
AX546394/c
LOCUS AX546394 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 53 from Patent EP1243289.
ACCESSION AX546394
VERSION AX546394.1 GI:25811585
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: EP 1243289-A 53 25-SEP-2002;
JOURNAL Methylgene, Inc. (CA)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160
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Db 23 AAAGTCTGTTACTACTACGACGG 1

RESULT 33
BD244922/c
LOCUS BD244922 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244922
KEYWORDS BD244922.1 GI:33054692
JP 2002528391-A/50.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 50 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/50
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
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PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1. .22
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FEATURES
source Location/Qualifiers
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Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
|||||
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 34
AX546305/c
LOCUS AX546305 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 54 from Patent EP1243290.
ACCESSION AX546305
VERSION AX546305.1 GI:25811496
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 54 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .22
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
|||||
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 35
AX546395/c
LOCUS AX546395 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 54 from Patent EP1243289.
ACCESSION AX546395
VERSION AX546395.1 GI:25811586
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 54 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
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Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 36
BD244905/c
LOCUS BD244905 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244905
VERSION BD244905.1 GI:33054675
KEYWORDS JP 2002528391-A/33.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 33 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/33
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC

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Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTCTGCTGCTC 36
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Db 20 CCCGCTGGTCTGCTGCTC 1

RESULT 37
BD244906/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244906
VERSION BD244906.1 GI:33054676
KEYWORDS JP 2002528391-A/34.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 34 03-SEP-2002;
METHYLGENE INC
OS Artificial Sequence
PN JP 2002528391-A/34
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCACTCGGTCTCAT 48
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Db 20 GCTGTCTCCACTCGGTCTCAT 1

RESULT 38
BD244907/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244907
VERSION BD244907.1 GI:33054677
KEYWORDS JP 2002528391-A/35.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 35 03-SEP-2002;
METHYLGENE INC
OS Artificial Sequence
PN JP 2002528391-A/35
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
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DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244907
VERSION BD244907.1 GI:33054677
KEYWORDS JP 2002528391-A/35.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 35 03-SEP-2002;
METHYLGENE INC
OS Artificial Sequence
PN JP 2002528391-A/35
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCACTCGGTCTCATCC 50
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Db 20 TGTCTCCACTCGGTCTCATCC 1

RESULT 39
BD244908/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244908
VERSION BD244908.1 GI:33054678
KEYWORDS JP 2002528391-A/36.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 36 03-SEP-2002;
METHYLGENE INC
OS Artificial Sequence
PN JP 2002528391-A/36
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
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FH Key 1. .20
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FT Location/Qualifiers
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AUTHORS		Besterman,J.M., Macleod,A.R. and Siders,W.M.	
TITLE		Modulation of gene expression by combination therapy	
JOURNAL		Patent: JP 2002528391-A 39 03-SEP-2002;	
COMMENT		METHYLGENE INC	
OS		Artificial Sequence	
PN		JP 2002528391-A/39	
PD		03-SEP-2002	
PF		19-OCT-1999 JP 2000576885	
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Query Match		1.2%; Score 20; DB 1; Length 20;	
Best Local Similarity		100.0%; Pred. No. 27;	
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		1504 CCAAGGAGGAGAGCCAGAA 1523	
Db		20 CCAAGGAGGAGAGCCAGAA 1	
RESULT 42			
BD244913/c			
LOCUS		BD244913 20 bp DNA linear PAT 17-JUL-2003	
DEFINITION		Modulation of gene expression by combination therapy.	
ACCESSION		BD244913	
VERSION		BD244913.1 GI:33054683	
KEYWORDS		JP 2002528391-A/41.	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 20)	
AUTHORS		Besterman,J.M., Macleod,A.R. and Siders,W.M.	
TITLE		Modulation of gene expression by combination therapy	
JOURNAL		Patent: JP 2002528391-A 41 03-SEP-2002;	
COMMENT		METHYLGENE INC	
OS		Artificial Sequence	
PN		JP 2002528391-A/41	
PD		03-SEP-2002	
PF		19-OCT-1999 JP 2000576885	
PR		19-OCT-1998 US 60/104804	
PI		JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC	
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706,			
PC			
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/09//			
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C12N5/10,C12N15/00,C12N5/00			
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FT		Location/Qualifiers	
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FEATURES		source	
Query Match		1.2%; Score 20; DB 1; Length 20;	
Best Local Similarity		100.0%; Pred. No. 27;	
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		41 TCGTCATCCTGAGAACACA 60	
Db		20 TCGTCATCCTGAGAACACA 1	
RESULT 41			
BD244911/c			
LOCUS		BD244911 20 bp DNA linear PAT 17-JUL-2003	
DEFINITION		Modulation of gene expression by combination therapy.	
ACCESSION		BD244911	
VERSION		BD244911.1 GI:33054681	
KEYWORDS		JP 2002528391-A/39.	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 20)	

Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCAGCTCTGGCTTC 1584
Db 20 CCTCTCAGCTCTGGCTTC 1

RESULT 43
BD244914/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244914
VERSION BD244914.1 GI:33054684
KEYWORDS JP 2002528391-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 42 03-SEP-2002;
METHYLENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/42
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 44
AX053077/c
LOCUS
DEFINITION Sequence 1 from Patent WO0071703.
ACCESSION AX053077
VERSION AX053077.1 GI:12227134
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 1 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 45
AX053086/c
LOCUS
DEFINITION Sequence 10 from Patent WO0071703.
ACCESSION AX053086
VERSION AX053086.1 GI:12227143
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 10 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions
1-4 and 17-20 are 2'-methoxyribose substituted
nucleotides; positions 5-16 are deoxyribonucleotides"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 46
AX456071/c
LOCUS
DEFINITION Sequence 1 from Patent WO0170675.
ACCESSION AX456071
VERSION AX456071.1 GI:21715026
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE Inhibitors of histone deacetylase
JOURNAL Patent: WO 0170675-A 1 27-SEP-2001;
Methylgene, Inc. (CA)
FEATURES
source
1..20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

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Db      20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 47
AX456072/c
LOCUS      20 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 2 from Patent WO0170675.
ACCESSION  AX456072
VERSION     AX456072.1  GI:21715027
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE      Inhibitors of histone deacetylase
JOURNAL    Patent: WO 0170675-A 2 27-SEP-2001;
            Methylgene, Inc. (CA)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
            |||||
Db      20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 48
AX456286/c
LOCUS      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 35 from Patent EP1243290.
ACCESSION  AX456286
VERSION     AX456286.1  GI:25811477
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    Patent: EP 1243290-A 35 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 CCCGCTGGTGTCTGTCTC 36
            |||||
Db      20 CCCGCTGGTGTCTGTCTC 1

RESULT 49
AX456287/c
LOCUS      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 36 from Patent EP1243290.
ACCESSION  AX456287
VERSION     AX456287.1  GI:25811478
KEYWORDS    synthetic construct
SOURCE      synthetic construct
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ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    Patent: EP 1243290-A 36 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 GCTGTCTCCCACTCGGTCA 48
            |||||
Db      20 GCTGTCTCCCACTCGGTCA 1

RESULT 50
AX546288/c
LOCUS      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 37 from Patent EP1243290.
ACCESSION  AX546288
VERSION     AX546288.1  GI:25811479
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    Patent: EP 1243290-A 37 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 TGTCTCCCACTCGGTCA 50
            |||||
Db      20 TGTCTCCCACTCGGTCA 1

RESULT 51
AX546289/c
LOCUS      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 38 from Patent EP1243290.
ACCESSION  AX546289
VERSION     AX546289.1  GI:25811480
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    Patent: EP 1243290-A 38 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
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/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTG 52
Db 20 TCTCCCACTCGGTCATCCTG 1

RESULT 52
AX546290/c
LOCUS AX546290 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 39 from Patent EP1243290.
ACCESSION AX546290
VERSION AX546290.1 GI:25811481
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 39 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTGAGACACA 60
Db 20 TCGGTCATCCTGAGACACA 1

RESULT 53
AX546292/c
LOCUS AX546292 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 41 from Patent EP1243290.
ACCESSION AX546292
VERSION AX546292.1 GI:25811483
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 41 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
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RESULT 54
AX546294/c
LOCUS AX546294 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 43 from Patent EP1243290.
ACCESSION AX546294
VERSION AX546294.1 GI:25811485
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 43 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 55
AX546295/c
LOCUS AX546295 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 44 from Patent EP1243290.
ACCESSION AX546295
VERSION AX546295.1 GI:25811486
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 44 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604
Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 56
AX546376/c
LOCUS AX546376 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 35 from Patent EP1243289.
ACCESSION AX546376
VERSION AX546376.1 GI:25811567
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
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REFERENCE
1
AUTHORS      Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE        Modulation of gene expression by combination therapy
JOURNAL      Patent: EP 1243289-A 35 25-SEP-2002;
              Methylgene, Inc. (CA)
FEATURES
  source
    1.20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTGCTGCTGCTC 36
Db 20 CCCGCTGGTGCTGCTGCTC 1

RESULT 57
AX546377/c
LOCUS      AX546377      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 36 from Patent EP1243289.
ACCESSION  AX546377
VERSION     AX546377.1 GI:25811568
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 36 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
  source
    1.20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCCACTCGGTCAT 48
Db 20 GCTGTCTCCCACTCGGTCAT 1

RESULT 58
AX546378/c
LOCUS      AX546378      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 37 from Patent EP1243289.
ACCESSION  AX546378
VERSION     AX546378.1 GI:25811569
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 37 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
  source
    1.20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide"
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Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCCACTCGGTCATCC 50
Db 20 TGTCTCCCACTCGGTCATCC 1

RESULT 59
AX546379/c
LOCUS      AX546379      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 38 from Patent EP1243289.
ACCESSION  AX546379
VERSION     AX546379.1 GI:25811570
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 38 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
  source
    1.20
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTG 52
Db 20 TCTCCCACTCGGTCATCCTG 1

RESULT 60
AX546380/c
LOCUS      AX546380      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 39 from Patent EP1243289.
ACCESSION  AX546380
VERSION     AX546380.1 GI:25811571
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 39 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
  source
    1.20
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTGAGACACA 60
Db 20 TCGGTCATCCTGAGACACA 1

RESULT 61
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AX546382/c
LOCUS AX546382 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 41 from Patent EP1243289.
ACCESSION AX546382
VERSION AX546382.1 GI:25811573
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 41 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
RESULT 62
AX546384/c
LOCUS AX546384 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 43 from Patent EP1243289.
ACCESSION AX546384
VERSION AX546384.1 GI:25811575
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 43 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1
RESULT 63
AX546385/c
LOCUS AX546385 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 44 from Patent EP1243289.
ACCESSION AX546385
VERSION AX546385.1 GI:25811576
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.

TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 44 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1585 TGCTGAGTCCCTCACGTTTC 1604
Db 20 TGCTGAGTCCCTCACGTTTC 1
RESULT 64
AX703613/c
LOCUS AX703613 20 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 17 from Patent WO03006652.
ACCESSION AX703613
VERSION AX703613.1 GI:29538512
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Li,Z., Bonfils,C. and Besterman,J.
TITLE Inhibition of specific histone deacetylase isoforms
JOURNAL Patent: WO 03006652-A 17 23-JAN-2003;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1585 TGCTGAGTCCCTCACGTTTC 1604
Db 20 TGCTGAGTCCCTCACGTTTC 1
RESULT 65
AX703614/c
LOCUS AX703614 20 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 18 from Patent WO03006652.
ACCESSION AX703614
VERSION AX703614.1 GI:29538513
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Li,Z., Bonfils,C. and Besterman,J.
TITLE Inhibition of specific histone deacetylase isoforms
JOURNAL Patent: WO 03006652-A 18 23-JAN-2003;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1585 TGCTGAGTCCCTCACGTTTC 1604
Db 20 TGCTGAGTCCCTCACGTTTC 1
RESULT 66
AX703614/c
LOCUS AX703614 20 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 18 from Patent WO03006652.
ACCESSION AX703614
VERSION AX703614.1 GI:29538513
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Li,Z., Bonfils,C. and Besterman,J.
TITLE Inhibition of specific histone deacetylase isoforms
JOURNAL Patent: WO 03006652-A 18 23-JAN-2003;
Methylgene, Inc. (CA)
FEATURES
source Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db 20 GGGTCAAGGAGGAGGTCAAG 1
|||||
RESULT 70
AX546381/c
LOCUS AX546381 linear DNA 20 bp PAT 26-NOV-2002
DEFINITION Sequence 40 from Patent EP1243289.
ACCESSION AX546381
VERSION AX546381.1 GI:25811572
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 40 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 62 CCTGACGCGTCTCTGTGACTC 81
|||||
Db 20 CCTGACGCGTCTCTGTGACTC 1
|||||
RESULT 71
AX546383/c
LOCUS AX546383 linear DNA 20 bp PAT 26-NOV-2002
DEFINITION Sequence 42 from Patent EP1243289.
ACCESSION AX546383
VERSION AX546383.1 GI:25811574
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 42 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1531 GGGTCAAGGAGGAGGCAAG 1550
|||||
Db 20 GGGTCAAGGAGGAGGTCAAG 1
|||||
RESULT 72
AX733295
LOCUS AX733295 linear DNA 17 bp PAT 08-MAY-2003
DEFINITION Sequence 4929 from Patent WO03025175.
ACCESSION AX733295
VERSION AX733295.1 GI:30512638
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4929 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 915 GATCGGTTAGTTGCTT 931
|||||
Db 1 GATCGGTTAGTTGCTT 17
|||||
RESULT 73
AX733529/c
LOCUS AX733529 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5163 from Patent WO03025175.
ACCESSION AX733529
VERSION AX733529.1 GI:30512872
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5163 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 902 CTCCTATCTGGGGATC 918
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Db 17 CTCCTATCTGGGGATC 1
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RESULT 74
BD244910/c
LOCUS BD244910 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244910
VERSION BD244910.1 GI:33054680
KEYWORDS JP 2002528391-A/38.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 38 03-SEP-2002;
```

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COMMENT      METHYLGENE INC
OS      Artificial Sequence
PN      JP 2002528391-A/38
PD      03-SEP-2002
PF      19-OCT-1999 JP 2000576885
PI      19-OCT-1998 US 60/104804
PR      JEFFREY M BESTERMAN, ALAN ROBERT MACLEOD, WILLIAM M SIDERS PC
A61K48/00, A61K31/165, A61K31/19, A61K31/513, A61K31/517, A61K31/PC
706,
PC
A61K31/7068, A61K31/7088, A61K31/7125, A61K45/00, A61P35/00, C12N15/PC
09//
PC      G12N5/10, C12N15/00, C12N5/00
CC      antisense
FH      key
FT      source
FT      Location/Qualifiers
          1..20
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      62 CCTGAGCGGTCTCTGTCATC 81
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DB      20 CCTGAGCGGTCTCTGTCATC 1

RESULT 75
AX462615
LOCUS      AX462615      20 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION      Sequence 359 from Patent EP1217079.
ACCESSION      AX462615
VERSION      AX462615.1 GI:24885828
KEYWORDS
SOURCE      Aegilops tauschii
ORGANISM      Aegilops tauschii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Aegilops.
REFERENCE      1
AUTHORS      Bernard, M., Sourdille, P. and Guyomarch, H.
TITLE      Microsatellite markers from Triticum tauschii
JOURNAL      Patent: EP 1217079-A 359 26-JUN-2002;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES
            source
            1..20
            /organism="Aegilops tauschii"
            /mol_type="unassigned DNA"
            /db_xref="taxon:37682"

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1187 GGAGAAGATCAACACAGCGAC 1206
      |||||
DB      1 GGAGAAAGCAACACAGCGAC 20

RESULT 76
AR029137/c
LOCUS      AR029137      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 13 from patent US 5859221.
ACCESSION      AR029137
VERSION      AR029137.1 GI:5941110
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
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REFERENCE      UNCLASSIFIED.
            1 (bases 1 to 20)
AUTHORS      Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE      2'-modified oligonucleotides
JOURNAL      Patent: US 5859221-A 13 12-JAN-1999;
FEATURES
            Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1507 AGGAGGAGAGCCAGAG 1524
      |||||
DB      19 AGGAGGAGAGCCAGCAG 2

RESULT 77
AR036521/c
LOCUS      AR036521      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 13 from patent US 5872232.
ACCESSION      AR036521
VERSION      AR036521.1 GI:5953189
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
            1 (bases 1 to 20)
            Cook, P. Dan. and Kawasaki, A. Mamoru.
            2'-O-modified oligonucleotides
            Patent: US 5872232-A 13 16-FEB-1999;
FEATURES
            Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1507 AGGAGGAGAGCCAGAG 1524
      |||||
DB      19 AGGAGGAGAGCCAGCAG 2

RESULT 78
AR073958/c
LOCUS      AR073958      20 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION      Sequence 27 from patent US 5952229.
ACCESSION      AR073958
VERSION      AR073958.1 GI:10000718
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
            1 (bases 1 to 20)
            Monia, B.P. and Boggs, R.T.
            Antisense oligonucleotide modulation of raf gene expression
            Patent: US 5952229-A 27 14-SEP-1999;
FEATURES
            Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1507 AGGAGGAGAGCCAGAG 1524
      |||||
DB      19 AGGAGGAGAGCCAGCAG 2
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RESULT 79
AR096054/c
LOCUS AR096054 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 13 from patent US 6005087.
ACCESSION AR096054
VERSION AR096054.1 GI:10024506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 6005087-A 13 21-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 80
AR105513/c
LOCUS AR105513 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6096720
ACCESSION AR105513
VERSION AR105513.1 GI:12819110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Love, W. Guy., Nicklin, P. Leslie., Hamilton, K. Ophelia. and Phillips, J. Ann.
TITLE Liposomal oligonucleotide compositions
JOURNAL Patent: US 6096720-A 13 01-AUG-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 81
E49537/c
LOCUS E49537 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Antisense oligonucleotide regulation of raft gene expression.
ACCESSION E49537
VERSION E49537.1 GI:18628118
KEYWORDS JP 2000152797-A/27.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Antisense oligonucleotide regulation of raft gene expression

JOURNAL Patent: JP 2000152797-A 27 06-JUN-2000;
COMMENT ISIS PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2000152797-A/27
PD 06-JUN-2000
PF 18-JAN-2000 JP 2000008654
PR 31-MAY-1994 US 08/250856
PI MONIA BURETTO P, BOGGUZU RUSSELL T
PC C12N15/09, A61K31/7088, A61K48/00, A61P17/06, A61P35/00, A61P43/00,
C12N15/00, A
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Homo sapiens (human)"
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 82
I27257/c
LOCUS I27257 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 27 from patent US 5563255.
ACCESSION I27257
VERSION I27257.1 GI:1818033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B. P. and Boggs, R. T.
TITLE Antisense oligonucleotide modulation of raf gene expression
JOURNAL Patent: US 5563255-A 27 08-OCT-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 83
AR212287/c
LOCUS AR212287 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6399754.
ACCESSION AR212287
VERSION AR212287.1 GI:21515821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook, P. Dan.
TITLE Sugar modified oligonucleotides
JOURNAL Patent: US 6399754-A 13 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..20

/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 84
AR215981/c
LOCUS AR215981 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 28 from patent US 6410518.
ACCESSION AR215981
VERSION AR215981.1 GI:23314269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P.
TITLE Antisense oligonucleotide inhibition of raf gene expression
JOURNAL Patent: US 6410518-A 28 25-JUN-2002;
FEATURES
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 85
AR231421/c
LOCUS AR231421 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6451991.
ACCESSION AR231421
VERSION AR231421.1 GI:27272504
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
TITLE Sugar-modified gapped oligonucleotides
JOURNAL Patent: US 6451991-A 13 17-SEP-2002;
FEATURES
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGCAG 2
RESULT 86
BD255496/c
LOCUS BD255496 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255496

BD255496.1 GI:33065266
JP 2002541795-A/3289.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3289 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3289
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
FT /organism="Eukaryote".
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1417 ACTTCACAAAAGCCCAAG 1433
Db 17 ACTTCACAAAAGCCCAAG 1
RESULT 87
BD255497/c
LOCUS BD255497 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255497
VERSION BD255497.1 GI:33065267
KEYWORDS JP 2002541795-A/3290.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3290 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3290
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH

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Key          Location/Qualifiers
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FT           /organism='Eukaryote'.

FEATURES
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            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAGGCCA 1431
Db 17 CAACTTCAATAAGCCA 1

RESULT 88
AR293317/c 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 5052 from patent US 6537751.
ACCESSION AR293317
VERSION AR293317.1 GI:31680601
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 5052 25-MAR-2003;
  source Location/Qualifiers
  1..18
  /organism='unknown'
  /mol_type='genomic DNA'

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1469 AGAGGAGAGAAAGGAA 1485
Db 17 AGAGGAGAGAAATGGAA 1

RESULT 89
AR035154/c 18 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 14 from patent US 5871730.
ACCESSION AR035154
VERSION AR035154.1 GI:5951822
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brzezinski,R., Dery,C.V. and Beaulieu,C.
TITLE Thermostable xylanase DNA, protein and methods of use
JOURNAL Patent: US 5871730-A 14 16-FEB-1999;
FEATURES Location/Qualifiers
  source 1..18
  /organism='unknown'
  /mol_type='unassigned DNA'

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 689 CATGACTGTGTCCTTCA 706
Db 18 CATGGCTGTGCCCTTCA 1

Key          Location/Qualifiers
FT - source  1..17
FT           /organism='Eukaryote'.

FEATURES
  source     Location/Qualifiers
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            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAGGCCA 1431
Db 17 CAACTTCAATAAGCCA 1

RESULT 88
AR293317/c 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 5052 from patent US 6537751.
ACCESSION AR293317
VERSION AR293317.1 GI:31680601
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 5052 25-MAR-2003;
  source Location/Qualifiers
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  /organism='unknown'
  /mol_type='genomic DNA'

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1469 AGAGGAGAGAAAGGAA 1485
Db 17 AGAGGAGAGAAATGGAA 1

RESULT 89
AR035154/c 18 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 14 from patent US 5871730.
ACCESSION AR035154
VERSION AR035154.1 GI:5951822
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brzezinski,R., Dery,C.V. and Beaulieu,C.
TITLE Thermostable xylanase DNA, protein and methods of use
JOURNAL Patent: US 5871730-A 14 16-FEB-1999;
FEATURES Location/Qualifiers
  source 1..18
  /organism='unknown'
  /mol_type='unassigned DNA'

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 689 CATGACTGTGTCCTTCA 706
Db 18 CATGGCTGTGCCCTTCA 1

RESULT 90
AR127642/c 18 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 60 from patent US 6180774.
ACCESSION AR127642
VERSION AR127642.1 GI:14114237
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and
TITLE Sanders,P.Rigden.
JOURNAL Synthetic DNA sequences having enhanced expression in
FEATURES monocolyledonous plants and method for preparation thereof
  source Patent: US 6180774-A 60 30-JAN-2001;
  Location/Qualifiers
  1..18
  /organism='unknown'
  /mol_type='unassigned DNA'

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 646 ATGTCACGGCGTGGAG 663
Db 18 ATGGTGGCGGCGTGGAG 1

RESULT 91
AR174568 18 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 23 from patent US 6307024.
ACCESSION AR174568
VERSION AR174568.1 GI:17914888
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
TITLE Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
JOURNAL Hammond,A.K.
FEATURES Cytokine zalphall1 Ligand
  source Patent: US 6307024-A 23 23-OCT-2001;
  Location/Qualifiers
  1..18
  /organism='unknown'
  /mol_type='unassigned DNA'

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGGCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 92
BD237586 18 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Cytokine receptor ZALPHALL1.
ACCESSION BD237586
VERSION BD237586.1 GI:33047356
KEYWORDS JP 2002526062-A/20.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
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AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor ZALPHA11
JOURNAL Patent: JP 2002526062-A 20 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526062-A/20
PD 20-AUG-2002
PF 23-SEP-1999 JP 2000574143
PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR
06-JUL-1999 US 09/347930
PI SCOTT R PRESNELL,DARRELL C CONKLIN,JULIA E NOVAK,ANGELA K PI
HAMMOND
PC C12N15/09,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/03,G01N33/53,G01N33/566,C12N15/00,
PC C12N5/00
CC Oligonucleotide primer ZC19954
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCCTGC 528
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACTGGGCTGGGGGACTGC 18
RESULT 93
BD237603
LOCUS Cytokine receptor ZALPHA11.
DEFINITION BD237603
ACCESSION BD237603.1 GI:33047373
VERSION JP 2002526062-A/37.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor ZALPHA11
JOURNAL Patent: JP 2002526062-A 37 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526062-A/37
PD 20-AUG-2002
PF 23-SEP-1999 JP 2000574143
PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR
06-JUL-1999 US 09/347930
PI SCOTT R PRESNELL,DARRELL C CONKLIN,JULIA E NOVAK,ANGELA K PI
HAMMOND
PC C12N15/09,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/02,G01N33/53,G01N33/566,C12N15/00,
PC C12N5/00
CC Oligonucleotide primer ZC19954
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCCTGC 528
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Db 1 ACTGGGCTGGGGGACTGC 18
RESULT 93
BD237603
LOCUS Cytokine receptor ZALPHA11.
DEFINITION BD237603
ACCESSION BD237603.1 GI:33047373
VERSION JP 2002526062-A/37.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor ZALPHA11
JOURNAL Patent: JP 2002526062-A 37 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526062-A/37
PD 20-AUG-2002
PF 23-SEP-1999 JP 2000574143
PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR
06-JUL-1999 US 09/347930
PI SCOTT R PRESNELL,DARRELL C CONKLIN,JULIA E NOVAK,ANGELA K PI
HAMMOND
PC C12N15/09,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/02,G01N33/53,G01N33/566,C12N15/00,
PC C12N5/00
CC Oligonucleotide primer ZC19954
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCCTGC 528
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Db 1 ACTGGGCTGGGGGACTGC 18
RESULT 94
BD248961
LOCUS Novel cytokine ZALPHA11 ligand.
DEFINITION BD248961
ACCESSION BD248961.1 GI:33058731
VERSION JP 2002537839-A/22.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 22 12-NOV-2002;
COMMENT OS Artificial Sequence
PN JP 2002537839-A/22
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
01-JUL-1999 US 60/142013
PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI
FOSTER,
PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
PI STACEY R DILLON,ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC19954
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
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Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCCTGC 528
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Db 1 ACTGGGCTGGGGGACTGC 18
RESULT 95
I75311/c
LOCUS Sequence 60 from patent US 5689052.
DEFINITION I75311
ACCESSION I75311
VERSION I75311.1 GI:3011452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and
Sanders,P.Rigden.

TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof
JOURNAL Patent: US 5689052-A 60 18-NOV-1997;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 646 ATGTCACGGCGTGAAG 663
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Db 18 ATGTCGCGCGTGAAG 1

RESULT 96
AR342894
LOCUS AR342894 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6576744.
ACCESSION AR342894
VERSION AR342894.1 GI:33738193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL Patent: US 6576744-A 22 10-JUN-2003;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
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Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 97
AR342911
LOCUS AR342911 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 39 from patent US 6576744.
ACCESSION AR342911
VERSION AR342911.1 GI:33738210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL Patent: US 6576744-A 39 10-JUN-2003;
FEATURES Location/Qualifiers
source 1. .18
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/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
|||||
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 98
AR374060
LOCUS AR374060 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6605272.
ACCESSION AR374060
VERSION AR374060.1 GI:40076632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 23 12-AUG-2003;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
|||||
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 99
AJ597665
LOCUS AJ597665 18 bp DNA linear PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 454G11.
ACCESSION AJ597665
VERSION AJ597665.1 GI:37947293
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 18)
AUTHORS Balzerque,S.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
FEATURES Location/Qualifiers
source 1. .18
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"

misc_feature /db_xref="taxon:3702"
/clone="454G11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1. .18
/note="T-DNA flanking sequence
left border"
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 593 GGAACGTGCTAAAGTATCA 610
Db 1 GGAACGTGCTAAAGTGTCA 18
RESULT 100
BD231175/c
LOCUS BD231175 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Antagonist based on receptor and prepration and utilization
methods.
ACCESSION BD231175
VERSION BD231175.1 GI:33040945
KEYWORDS JP 2002525119-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stahl,N. and Yancopoulos,G.D.
TITLE Antagonist based on receptor and prepration and utilization methods
JOURNAL Patent: JP 2002525119-A 1 13-AUG-2002;
REGENERON PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002525119-A/1
PD 13-AUG-2002
PF 22-SEP-1999 JP 2000572379
PR 25-SEP-1998 US 60/101858,19-MAY-1999 US 09/313942 PI
NEIL STAHL,GEORGE D YANCOPOULOS
PC C12N15/09,C07K14/715,C07K19/00,C12N1/19,C12N1/21,C12N5/10, PC
C12P21/02//
PC A61K38/00,A61P19/10,A61P35/00,(C12P21/02,C12R1:91),C12N15/00,
PC C12N5/00,
PC A61K37/02
CC Kozak sequence
FH Key
FT source
FT Location/Qualifiers
1. .16
/organism="Artificial Sequence".
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGACGGCG 1
RESULT 101
AR242277/c
LOCUS AR242277 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6472179.
ACCESSION AR242277
VERSION AR242277.1 GI:27288127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)

AUTHORS Stahl,N. and Yancopoulos,G.D.
TITLE Receptor based antagonists and methods of making and using
JOURNAL Patent: US 6472179-A 3 29-OCT-2002;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGACGGCG 1
RESULT 102
AR328425
LOCUS AR328425 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5827 from patent US 6566127.
ACCESSION AR328425
VERSION AR328425.1 GI:33714233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5827 20-MAY-2003;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CTGGGGGCGCTGCACCA 16
RESULT 103
AX503577/c
LOCUS AX503577 16 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 3 from Patent EP1229047.
ACCESSION AX503577
VERSION AX503577.1 GI:23385865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Yancopoulos,G.D. and Stahl,N.
TITLE Il-1 receptor fusion proteins used as antagonists and methods of
making and using
JOURNAL Patent: EP 1229047-A 3 07-AUG-2002;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Kozak sequence"
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGACGGCG 1

RESULT 104
BD255495/c
LOCUS BD255495 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255495
VERSION BD255495.1 GI:33065265
KEYWORDS JP 2002541795-A/3288.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3288 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC

COMMENT OS Eukaryote
PN JP 2002541795-A/3288
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1418 CTTCAAAAAGCCAG 1433
Db 17 CTTCAAAATAGCCAG 2

RESULT 105
BD255498/c
LOCUS BD255498 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255498
VERSION BD255498.1 GI:33065268
KEYWORDS JP 2002541795-A/3291.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3291 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC

COMMENT OS Eukaryote
PN JP 2002541795-A/3291
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390

PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAGCC 1430
Db 16 CAACTTCAAAATAGCC 1

RESULT 106
AR327352
LOCUS AR327352 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4754 from patent US 6566127.
ACCESSION AR327352
VERSION AR327352.1 GI:33713160
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., Mcswiggen, J. A., Stinchcomb, D. T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4754 20-MAY-2003;
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source
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/organism='unknown'
/mol_type='unassigned RNA'

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGCCTGCACCA 532
Db 1 CTGGGAGCCTGCACCA 16

RESULT 107
AX217646/c
LOCUS AX217646 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3088 from Patent WO0159103.
ACCESSION AX217646
VERSION AX217646.1 GI:15527707
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., Mcswiggen, J. and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 3088 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

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McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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      /organism="synthetic construct"
      /mol_type="unassigned RNA"
      /db_xref="taxon:32630"
      /note="Nucleic Acid"

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1119 TTTGGACCAGATTTC A 1134
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Db 17 TTTGGACCAGATTGCA 2

RESULT 108
AX218225/c
LOCUS AX218225 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3667 from Patent WO0159103.
ACCESSION AX218225
VERSION AX218225.1 GI:15528286
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 3667 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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      /db_xref="taxon:32630"
      /note="Nucleic Acid"

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1119 TTTGGACCAGATTTC A 1134
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Db 16 TTTGGACCAGATTGCA 1

RESULT 109
AX475558/c
LOCUS AX475558 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 779 from Patent WO0224750.
ACCESSION AX475558
VERSION AX475558.1 GI:22214843
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 779 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
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Db 17 AAACCAAGGAGGAGCA 2

RESULT 110
AX475559/c
LOCUS AX475559 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 780 from Patent WO0224750.
ACCESSION AX475559
VERSION AX475559.1 GI:22214844
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 780 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCAAACGCGCGGATT 1262
    |||||
Db 17 CCAAATGCGCGGATT 2

RESULT 111
AX784017/c
LOCUS AX784017 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2348 from Patent WO03050284.
ACCESSION AX784017
VERSION AX784017.1 GI:32951866
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2348 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
  source
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
    |||||
Db 17 AAACCAAGGAGGAGCA 2

RESULT 112
AX784018/c
LOCUS AX784018 17 bp DNA linear PAT 17-JUL-2003
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DEFINITION Sequence 2349 from Patent WO03050284.
ACCESSION AX784018
VERSION AX784018.1 GI:32951867
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2349 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1501 AAACCAAGGAGGAGAA 1516
Db 16 AAACCAAGGAGGAGCA 1
RESULT 113
AR267656
LOCUS AR267656 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 46 from patent US 6497880.
ACCESSION AR267656
VERSION AR267656.1 GI:29697764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wisniewski, J.
TITLE Heat shock genes and proteins from Neisseria meningitidis, Candida glabrata and Aspergillus fumigatus
JOURNAL Patent: US 6497880-A 46 24-DEC-2002;
FEATURES
source
1.18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 283 AAGCCAATGCTGAGGA 298
Db 2 AAGCCAATGCCGAGGA 17
RESULT 114
AR292367
LOCUS AR292367 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4102 from patent US 6537751.
ACCESSION AR292367
VERSION AR292367.1 GI:31679651
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4102 25-MAR-2003;
FEATURES
Location/Qualifiers

source
1.18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCTCTGGGCTCTCTG 16
Db 1 ATGCTCTGGTGTCTCTG 16
RESULT 115
AR297444
LOCUS AR297444 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9179 from patent US 6537751.
ACCESSION AR297444
VERSION AR297444.1 GI:31684728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9179 25-MAR-2003;
FEATURES
source
1.18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1457 AGAGAAAGACCCAGAG 1472
Db 1 AGAGAAAGAACCCAGAG 16
RESULT 116
BD057516/c
LOCUS BD057516 Cytokine 7 receptor.
DEFINITION BD057516
ACCESSION BD057516.1 GI:22603122
VERSION JP 2001514493-A/3.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lok, S., Kho, C.J., Jelmborg, A.C., Adams, R.L., Whitmore, T.E. and Farrah, T.M.
TITLE Cytokine 7 receptor
JOURNAL Patent: JP 2001514493-A 3 11-SEP-2001;
ZymoGenetics Inc
COMMENT PN JP 2001514493-A/3
PD 11-SEP-2001
PF 18-FEB-1998 JP 1998536782
PR 20-FEB-1997 US 08/803305,02-OCT-1997 US 08/943087 PI
SI LOK, CHOON J KHO, ANNA C JELMBERG, ROBYN L ADAMS, THEODORE E PI WHITMORE,
PI THERESA M FARRAH
PC C12N15/12, C07K14/715, C12N15/62, C07K16/28, C07K16/42, C07K19/00,
PC G01N33/50
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FEATURES
source
1.18
/organism="synthetic construct"

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
Db 17 AAAGAGAAACACCCAG 2

RESULT 117
AX727187/c
LOCUS AX727187 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4874 from Patent WO03025176.
ACCESSION AX727187
VERSION AX727187.1 GI:30506530
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Telesman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4874 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 AATGCTGAGGAGAT 301
Db 15 AATGCTGAGGAGAT 2

RESULT 118
AX784019/c
LOCUS AX784019 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2350 from Patent WO03050284.
ACCESSION AX784019
VERSION AX784019.1 GI:32951868
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2350 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAG 1514
Db 15 AAACCAAGGAGGAG 2

Db 15 AAACCAAGGAGGAG 2

RESULT 119
AX784020/c
LOCUS AX784020 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2351 from Patent WO03050284.
ACCESSION AX784020
VERSION AX784020.1 GI:32951869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2351 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAG 1514
Db 14 AAACCAAGGAGGAG 1

RESULT 120
A12195
LOCUS A12195 17 bp DNA linear PAT 10-DEC-1993
DEFINITION EBI 782.
ACCESSION A12195
VERSION A12195.1 GI:491298
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Heckl, K., Spevak, W., Ostermann, E., Zoepfel, A., Krystek, E.,
Maurer-Fogy, I., Wiche-Castanon, M.J., Stratowa, C. and Hauptmann, R.
TITLE Human manganese superoxide dismutase (hMn-SOD)
JOURNAL Patent: EP 0282899-A 18 21-SEP-1988;
BOEHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 857 GGAGATGTTCCAGCCTA 873
Db 1 GGAGATGTTACAGCCCA 17

RESULT 121
A26903/c
LOCUS A26903 17 bp DNA linear PAT 05-JUN-1995
DEFINITION Primer 10.
ACCESSION A26903
VERSION A26903.1 GI:1248331
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
REFERENCE artificial sequences.
1 (bases 1 to 17)
AUTHORS
TITLE IMPROVEMENTS IN OLIGONUCLEOTIDE PRIMERS AND PROBES
JOURNAL Patent: WO 9305176-A 19 18-MAR-1993;
FEATURES Location/Qualifiers
source
1.17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CAAGGAGGAGGCAAGT 1551
Db 17 CAAAAGGAGGCAAGT 1

RESULT 122
AR158444/c
LOCUS AR158444 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 66 from patent US 6251588.
ACCESSION AR158444
VERSION AR158444.1 GI:16220483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 66 26-JUN-2001;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTGGGGTCTCTGCC 19
Db 17 GTCTGGGTCACTGCC 1

RESULT 123
BD254323/c
LOCUS BD254323 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254323
VERSION BD254323.1 GI:33064093
KEYWORDS JP 2002541795-A/2116.
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2116 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2116
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,

PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1.17
FT /organism='Eukaryote'.
FEATURES Location/Qualifiers
source
1.17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 CCTGAGAACACAGCCTG 65
Db 17 CCTGAGAGACAGGCTG 1

RESULT 124
AR186914
LOCUS AR186914 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2402 from patent US 6346398.
ACCESSION AR186914
VERSION AR186914.1 GI:20232879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2402 12-FEB-2002;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAAACTT 482
Db 1 CAACTGCTTTGAAACTT 17

RESULT 125
AR190268/c
LOCUS AR190268 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5756 from patent US 6346398.
ACCESSION AR190268
VERSION AR190268.1 GI:20236233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5756 12-FEB-2002;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGCTGC 34
| | | | | | | | | | | | | | | |
Db 17 CTGCTGGTGTGCTGCTGC 1

RESULT 126
AR195652
LOCUS AR195652 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 117 from patent US 6350934.
ACCESSION AR195652
VERSION AR195652.1 GI:20245089
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 117 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 495 ACGACATCGCCGTGAA 511
| | | | | | | | | | | | | | | |
Db 1 AAGTACATCGCCGTGAA 17

RESULT 127
AR323545
LOCUS AR323545 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 947 from patent US 6566127.
ACCESSION AR323545
VERSION AR323545.1 GI:33709353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 947 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAAACTT 482
| | | | | | | | | | | | | | | |
Db 1 CAAGTGTGTGAAACTT 17

RESULT 128
AR325233/c
LOCUS AR325233 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 2635 from patent US 6566127.
ACCESSION AR325233

VERSION AR325233.1 GI:33711041
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2635 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGCTGC 34
| | | | | | | | | | | | | | | |
Db 17 CTGCTGGTGTGCTGCTGC 1

RESULT 129
AR327353
LOCUS AR327353 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 4755 from patent US 6566127.
ACCESSION AR327353
VERSION AR327353.1 GI:33713161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4755 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGCGCTGCACCATG 534
| | | | | | | | | | | | | | | |
Db 1 TGGGAGCCTGCACCAAG 17

RESULT 130
AR327354
LOCUS AR327354 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 4756 from patent US 6566127.
ACCESSION AR327354
VERSION AR327354.1 GI:33713162
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4756 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCCTGCACCATGCAA 537
1 GAGCCTGCACCAAGCAA 17

Db

RESULT 131
AR327355
LOCUS AR327355 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4757 from patent US 6566127.
ACCESSION AR327355
VERSION AR327355.1 GI:33713163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4757 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAAG 539
1 GCCTGCACCAAGCAAG 17

Db

RESULT 132
AR327356
LOCUS AR327356 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4758 from patent US 6566127.
ACCESSION AR327356
VERSION AR327356.1 GI:33713164
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4758 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAAGA 540
1 CCTGCACCAAGCAAGGA 17

Db

RESULT 133
AR327992/c
LOCUS AR327992 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5394 from patent US 6566127.
ACCESSION AR327992
VERSION AR327992.1 GI:33713800

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5394 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGTGAGGACTGTCC 412
17 GGTGGAGAGGACTGTCC 1

Db

RESULT 134
AR363927
LOCUS AR363927 17 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 22 from patent US 5240847.
ACCESSION AR363927
VERSION AR363927.1 GI:34426034
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Heckl,K., Spevak,W., Ostermann,E., Zophel,A., Krystek,E., Maurer-Fogy,I., Wiche-Castanon,M.J., Stratowa,C. and Hauptmann,R.
TITLE Human manganese superoxide dismutase (hMn-SOD)
JOURNAL Patent: US 5240847-A 22 31-AUG-1993;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 857 GGAGATGTTCCAGCCTA 873
1 GGAGATGTTACAGCCCA 17

Db

RESULT 135
AX037535/c
LOCUS AX037535 17 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 160 from Patent WO0056922.
ACCESSION AX037535
VERSION AX037535.1 GI:11226962
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and Sanders,R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 160 28-SEP-2000;
NORBERG LEIF TORBJORN (SE); OLAISSON ERIK (SE); JONSSON LENA (SE); GEMINI GENOMICS AB (SE); LINDSTROM PER HARRY RUTGER (SE); SANDERS RHIANNON (SE)
FEATURES
source Location/Qualifiers
1..17

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 12 CTCTGCCCGCTGGTGCT 28
Db 17 CTGTGCCCGCTGCTGCT 1

RESULT 136
AX272526
LOCUS AX272526 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 95 from Patent WO0162911.
ACCESSION AX272526
VERSION AX272526.1 GI:16545263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 95 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 1562 GGACTTCTCCAGCTGTG 1578
Db 1 GGACTTCTCCATCTCTG 17

RESULT 137
AX422324
LOCUS AX422324 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 660 from Patent WO0188124.
ACCESSION AX422324
VERSION AX422324.1 GI:21525706
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 660 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 298 AGATGACCAAGTACCAC 314
Db 1 AGATGACCAAGGACGAC 17

RESULT 138
AX422476
LOCUS AX422476 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 812 from Patent WO0188124.
ACCESSION AX422476
VERSION AX422476.1 GI:21525858
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 812 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 142 TCTGTACTACTACGAC 158
Db 1 TCCGTACTACTATGAC 17

RESULT 139
AX475000
LOCUS AX475000 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 221 from Patent WO0224750.
ACCESSION AX475000
VERSION AX475000.1 GI:22214285
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang,J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 221 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 1583 CCTGCTGAGTCCCTCAC 1599
Db 1 CCTGCTGACTCCACAC 17

RESULT 140
AX499281
LOCUS AX499281 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 588 from Patent EP1229046.
ACCESSION AX499281

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VERSION      AX499281.1  GI:23381574
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Zhan,J.
TITLE        Human testis expressed patched like protein
JOURNAL      Patent: EP 1229046-A 588 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES
  source     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY          1456 AAGAGAAAGACCCAGAG 1472
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Db          1 AAGAGGAAGACCTAGAG 17

RESULT 141
AX499282
LOCUS       AX499282
DEFINITION Sequence 589 from Patent EP1229046.
ACCESSION  AX499282
VERSION    AX499282.1  GI:23381575
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 589 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES
  source     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY          1457 AGAGAAAGACCCAGAGG 1473
          ||||| ||||| ||||| |||||
Db          1 AGAGGAAGACCTAGAGG 17

RESULT 142
AX499283
LOCUS       AX499283
DEFINITION Sequence 590 from Patent EP1229046.
ACCESSION  AX499283
VERSION    AX499283.1  GI:23381576
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 590 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES
  source     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY          1458 GAGAAAGACCCAGAGGA 1474
          ||||| ||||| ||||| |||||
Db          1 GAGGAGACCTAGAGGA 17

RESULT 143
AX499284
LOCUS       AX499284
DEFINITION Sequence 591 from Patent EP1229046.
ACCESSION  AX499284
VERSION    AX499284.1  GI:23381577
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 591 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES
  source     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY          1459 AGAAAGACCCAGAGGAG 1475
          ||||| ||||| ||||| |||||
Db          1 AGGAAGACCTAGAGGAG 17

RESULT 144
AX578270/c
LOCUS       AX578270
DEFINITION Sequence 108 from Patent WO0211674.
ACCESSION  AX578270
VERSION    AX578270.1  GI:27647472
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
             and Grupe,A.
TITLE       Method and reagent for the inhibition of calcium activated chloride
             channel-1 (clca-1)
JOURNAL     Patent: WO 0211674-A 108 14-FEB-2002;
             RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
             Thompson, James (US)
FEATURES
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             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned RNA"
             /db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
```


REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 1507 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 998 GATGCTGGGAGCGGTG 1014 17 bp DNA linear PAT 08-MAY-2003
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Db 1 GATCCTGGGAGCGGAG 17
RESULT 150
AX736944/c
LOCUS AX736944 Sequence 2534 from Patent WO03025177.
ACCESSION AX736944
VERSION AX736944.1 GI:30516232
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 2534 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1550 GTTGGCCTGAATGGACC 1566
|||||
Db 17 GTTGGCATGAATGGATC 1
RESULT 151
AX738376
LOCUS AX738376 Sequence 3966 from Patent WO03025177.
ACCESSION AX738376
VERSION AX738376.1 GI:30517664
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 3966 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1573 GCTCTGGCTTCCTGCTG 1589
|||||
Db 1 GATCTGCTTCCTGCTG 17
RESULT 152
AX759597/c
LOCUS AX759597 Sequence 2918 from Patent WO03040369.
DEFINITION AX759597
ACCESSION AX759597
VERSION AX759597.1 GI:32254213
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2918 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 717 GAGTACTTCCCAGGAAC 733
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Db 17 GAGAACTTCCCAGGATC 1
RESULT 153
AX759648/c
LOCUS AX759648 Sequence 2969 from Patent WO03040369.
DEFINITION AX759648
ACCESSION AX759648
VERSION AX759648.1 GI:32254264
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2969 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 15; Conservative 0

QY 902 CTCCTATCTGGGATC 918
Db 17 CTTCTGTCTGGGATC 1

RESULT 154
AX783524/c
LOCUS AX783524 17 bp DNA PAT 17-JUL-2003
DEFINITION Sequence 1855 from Patent WO03050284.
ACCESSION AX783524
VERSION AX783524.1 GI:32951373
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 1855 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1508 GGAGGAGAGCCAGAG 1524
Db 17 GGAGGAGAGCCAGAG 1

RESULT 155
AX783525/c
LOCUS AX783525 17 bp DNA PAT 17-JUL-2003
DEFINITION Sequence 1856 from Patent WO03050284.
ACCESSION AX783525
VERSION AX783525.1 GI:32951374
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 1856 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAA 1523
Db 17 AGGAGGAGAGCCAGCA 1

RESULT 156
AX784014/c
LOCUS AX784014 17 bp DNA PAT 17-JUL-2003

DEFINITION Sequence 2345 from Patent WO03050284.
ACCESSION AX784014
VERSION AX784014.1 GI:32951863
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2345 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCA 1520
Db 17 CCAAGGAGGAGCAACCA 1

RESULT 157
AX784015/c
LOCUS AX784015 17 bp DNA PAT 17-JUL-2003
DEFINITION Sequence 2346 from Patent WO03050284.
ACCESSION AX784015
VERSION AX784015.1 GI:32951864
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2346 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1503 ACCAGGAGGAGAGGCC 1519
Db 17 ACCAGGAGGAGCAACC 1

RESULT 158
AX784016/c
LOCUS AX784016 17 bp DNA PAT 17-JUL-2003
DEFINITION Sequence 2347 from Patent WO03050284.
ACCESSION AX784016
VERSION AX784016.1 GI:32951865
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1

JOURNAL Patent: WO 03050284-A 2347 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGGAGC 1518
Db
17 AACCAAGGAGGAGCAAC 1

RESULT 159
BD104867/c
LOCUS
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104867
VERSION BD104867.1 GI:22650441
KEYWORDS WO 0192572-A/971.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 971 06-DEC-2001;
NISSHINO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA

COMMENT OS Artificial Sequence
PN WO 0192572-A/971
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC Cl2Q1/68,Cl2M1/00,Cl2N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1. .17
/organism='Artificial Sequence'.
FT Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CACTCGGTCATCCTGAG 54
Db
17 CACTCGGTCAGCCTGTG 1

RESULT 160
BD197713/c
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD197713
VERSION BD197713.1 GI:33007483
KEYWORDS JP 2002509721-A/739.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
Patent: JP 2002509721-A 739 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/739
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT, PI JAMES A MCSWIGGEN
PC Cl2N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC A61P29/00,
PC A61P35/00,A61P43/00,Cl2N5/10,Cl2N9/00//A61K35/76,Cl2N15/00, PC Cl2N5/00
CC Method and reagent for treating diseases or conditions CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1. .17
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1375 ATTCGAGGAGGAGGGA 1391
Db
17 ATTCGAGGAGGAGGGA 1

RESULT 161
AR435876/c
LOCUS
DEFINITION Sequence 135 from patent US 6656731.
ACCESSION AR435876
VERSION AR435876.1 GI:40198960
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
1 (bases 1 to 16)
REFERENCE Eckstein,F., Ludwig,J. and Beigelman,L.
AUTHORS Nucleic acid catalysts with endonuclease activity
TITLE Patent: US 6656731-A 135 02-DEC-2003;
JOURNAL Location/Qualifiers
FEATURES
source
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 321 GACTACATTAAATTC 335
Db
16 GACTACATTAAATTC 2

RESULT 162
AR043790
LOCUS
DEFINITION Sequence 160 from patent US 5814517.
14 bp DNA
AR043790 linear PAT 29-SEP-1999

Query Match	0.8%; Score 13; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 83;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 721 ACTTCCCAGGAAC 733	
Db 1 ACTTCCCAGGAAC 13	
RESULT 165	
A58492	
LOCUS	15 bp DNA linear PAT 05-MAR-1998
DEFINITION	Sequence 2 from Patent WO9637605.
ACCESSION	A58492
VERSION	A58492.1 GI:3714127
KEYWORDS	
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1
TITLE	Pirotzky, E. and Colote, S.
JOURNAL	ANTI SENSE OLIGONUCLEOTIDES FOR BLOCKING IGE RECEPTOR SYNTHESIS
COMMENT	Patent: WO 9637605-A 2 28-NOV-1996;
FEATURES	SOD CONSEILS RECH APPLIC (FR)
source	Other publication AU 6008296 961211.
	Location/Qualifiers
	1. .15
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 96;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865	
Db 1 TAATGGAGATGTT 13	
RESULT 166	
A58495	
LOCUS	15 bp DNA linear PAT 05-MAR-1998
DEFINITION	Sequence 5 from Patent WO9637605.
ACCESSION	A58495
VERSION	A58495.1 GI:3714130
KEYWORDS	
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1
TITLE	Pirotzky, E. and Colote, S.
JOURNAL	ANTI SENSE OLIGONUCLEOTIDES FOR BLOCKING IGE RECEPTOR SYNTHESIS
COMMENT	Patent: WO 9637605-A 5 28-NOV-1996;
FEATURES	SOD CONSEILS RECH APPLIC (FR)
source	Other publication AU 6008296 961211.
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	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 96;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865	
Db 1 TAATGGAGATGTT 13	
RESULT 167	
A88175/c	

LOCUS A88175 15 bp DNA linear PAT 23-JAN-2000
DEFINITION Sequence 323 from Patent WO9833904.
ACCESSION A88175
VERSION A88175.1 GI:6736745
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 323 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAAGAGGAGG 1389
Db 13 TCTGAAGAGGAGG 1
RESULT 168
A90142/C
LOCUS A90142 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 323 from Patent EP0856579.
ACCESSION A90142
VERSION A90142.1 GI:6738656
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 323 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAAGAGGAGG 1389
Db 13 TCTGAAGAGGAGG 1
RESULT 169
AR070443
LOCUS AR070443 15 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5892023.
ACCESSION AR070443
VERSION AR070443.1 GI:7221331
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pirotzky,E. and Colote,S.
TITLE Anti sense oligonucleotides for blocking IgE receptor synthesis
JOURNAL Patent: US 5892023-A 2 06-APR-1999;
FEATURES
Location/Qualifiers

source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865
Db 1 TAATGGAGATGTT 13
RESULT 170
AR070446
LOCUS AR070446 15 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5892023.
ACCESSION AR070446
VERSION AR070446.1 GI:7221334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pirotzky,E. and Colote,S.
TITLE Anti sense oligonucleotides for blocking IgE receptor synthesis
JOURNAL Patent: US 5892023-A 5 06-APR-1999;
FEATURES
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865
Db 1 TAATGGAGATGTT 13
RESULT 171
I61704
LOCUS I61704 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 258 from patent US 5658780.
ACCESSION I61704
VERSION I61704.1 GI:2479652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 258 19-AUG-1997;
FEATURES
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1045 GGACATATGAGAC 1057
Db 2 GGACATATGAGAC 14
RESULT 172
AR180305
LOCUS AR180305 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 373 from patent US 6333152.
FEATURES
Location/Qualifiers

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ACCESSION AR180305
VERSION AR180305.1 GI:20222338
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 633152-A 373 25-DEC-2001;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 513 TGGGCTGGGGGCC 525
Db 3 TGGGCTGGGGGCC 15
RESULT 173
AX572210/c
LOCUS AX572210 15 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 250 from Patent WO02055741.
ACCESSION AX572210
VERSION AX572210.1 GI:26004300
KEYWORDS Human immunodeficiency virus
SOURCE Human immunodeficiency virus
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
JOURNAL Patent: WO 02055741-A 250 18-JUL-2002;
INNOGENETICS N.V. (BE)
FEATURES
source
1. .15
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1273 CCATCCCTGAGGA 1285
Db 15 CCATCCCTGAGGA 3
RESULT 174
AX636172
LOCUS AX636172 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3311 from Patent EP1260586.
ACCESSION AX636172
VERSION AX636172.1 GI:28471786
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulich-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
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Genes
JOURNAL Patent: EP 1260586-A 3311 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1045 GGACATATGAGAC 1057
Db 2 GGACATATGAGAC 14
RESULT 175
BD065688/c
LOCUS BD065688 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065688
VERSION BD065688.1 GI:22611291
KEYWORDS JP 2001511000-A/323.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 323 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/323
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FEATURES
source
1. .15
/organism="Unknown"
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1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAGAGGAGG 1389
Db 13 TCTGAGAGGAGG 1
RESULT 176
AR010015
LOCUS AR010015 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 27 from patent US 5756684.
ACCESSION AR010015
VERSION AR010015.1 GI:3968820
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 27 26-MAY-1998;
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FEATURES
source Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1383 GAGGAGGAGG 1395
|||||
Db 2 GAGGAGGAGG 14

RESULT 177
AR034750
LOCUS AR034750 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5869622.
ACCESSION AR034750
VERSION AR034750.1 GI:5950355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 27 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1383 GAGGAGGAGG 1395
|||||
Db 2 GAGGAGGAGG 14

RESULT 178
AR096597/c
LOCUS AR096597 16 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 27 from patent US 608045.
ACCESSION AR096597
VERSION AR096597.1 GI:10025536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Copeland,W.C. and Wang,T.S.-F.
TITLE Nucleic acid encoding human DNA polymerase .alpha
JOURNAL Patent: US 608045-A 27 28-DEC-1999;
FEATURES Location/Qualifiers
source 1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTCTGCCCCGCTGG 24
|||||
Db 16 CTCTGCCCCGCTGG 4

RESULT 179
AR105973/c
LOCUS AR105973 16 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 27 from patent US 6103473.
ACCESSION AR105973
VERSION AR105973.1 GI:12820038
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Copeland,W.C. and Wang,T.S.-F.
TITLE Mutagenicity screening method using human DNA polymerase or catalytic polypeptide
JOURNAL Patent: US 6103473-A 27 15-AUG-2000;
FEATURES Location/Qualifiers
source 1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTCTGCCCCGCTGG 24
|||||
Db 16 CTCTGCCCCGCTGG 4

RESULT 180
AX327134/c
LOCUS AX327134 16 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 330 from Patent WO0178894.
ACCESSION AX327134
VERSION AX327134.1 GI:18097846
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Keith,T.
TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
JOURNAL Patent: WO 0178894-A 330 25-OCT-2001;
Genome Therapeutics Corp. (US)
FEATURES Location/Qualifiers
source 1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGGACTGTCCAGT 415
|||||
Db 13 AGGACTGTCCAGT 1

RESULT 181
A18727/c
LOCUS A18727 16 bp DNA linear PAT 18-APR-1994
DEFINITION kozak consensus leader sequence.
ACCESSION A18727
VERSION A18727.1 GI:513378
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Peakman,T.C., Page,M.J. and Charles,I.G.
TITLE Baculoviral expression system comprising procaryotic leader sequence
JOURNAL Patent: EP 0486170-A 2 20-MAY-1992;

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FEATURES
  source
    THE WELLCOME FOUNDATION LIMITED
    Location/Qualifiers
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      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 644 CCATGGTGACGGCGTG 659
Db 16 CCATGGTGCGCGCGG 1

RESULT 182
LOCUS A29549 16 bp DNA linear PAT 12-JUN-1995
DEFINITION Oligonucleotide probe.
ACCESSION A29549
VERSION A29549.1 GI:1248955
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Mackellar,W.C. and Robey,C.S.
TITLE An improved method for folding tissue plasminogen activators and
  derivatives thereof
JOURNAL Patent: EP 0523296-A 18 20-JAN-1993;
  ELI LILLY AND COMPANY
FEATURES
  source
    Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 464 GGCAAGTGCTGTGAAA 479
Db 1 GCGAAGTCCTGTGAAA 16

RESULT 183
LOCUS A42606 16 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 124 from Patent WO9502051.
ACCESSION A42606
VERSION A42606.1 GI:2298055
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unidentified
    unclassified.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
  Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
  PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
  CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 124 19-JAN-1995;
  BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT Other publication AU 7345694 950206.
FEATURES
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      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 184
LOCUS A88795 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 943 from Patent WO9833904.
ACCESSION A88795
VERSION A88795.1 GI:6737365
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unidentified
    unclassified.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 943 06-AUG-1998;
  BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 185
LOCUS AR072525 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 22 from patent US 5948616.
ACCESSION AR072525
VERSION AR072525.1 GI:9999289
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Chao,L. and Chao,J.
TITLE Methods and compositions of correlating tissue kallikrein gene
  promoter polymorphisms with essential hypertension
JOURNAL Patent: US 5948616-A 22 07-SEP-1999;
  Location/Qualifiers
FEATURES
  source
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      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
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  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGGC 1400
Db 1 GGAGGGGGGGGGGGGC 16

RESULT 186
LOCUS BD244651 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Low temperature-adaptable equine influenza virus.
ACCESSION BD244651
VERSION BD244651.1 GI:33054421
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REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 11 26-NOV-2002;
FEATURES location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1184 CCTGGAGAGATCAAA 1199
Db 1 CCAGCAGAGATCAAA 16

RESULT 191
AR328586 AR328586 16 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 5988 from patent US 6566127.
ACCESSION AR328586
VERSION AR328586.1 GI:33714394
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5988 20-MAY-2003;
FEATURES location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAACT 481
Db 1 CAACTGCTTTGAACT 16

RESULT 192
AR343259 AR343259 16 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 35 from patent US 6579528.
ACCESSION AR343259
VERSION AR343259.1 GI:33738777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6579528-A 35 17-JUN-2003;
FEATURES location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCAA 571
Db 1 GCATCTGTTAAGTCAA 16

RESULT 193
AR367752 AR367752 16 bp DNA linear PAT 12-SEP-2003
LOCUS
DEFINITION Sequence 22 from patent US 6376182.
ACCESSION AR367752
VERSION AR367752.1 GI:34601131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chao,L., Chao,J. and Song,Q.
TITLE Methods and compositions for correlating tissue kallikrein gene promoter polymorphisms with treatment of essential hypertension
JOURNAL Patent: US 6376182-A 22 23-APR-2002;
FEATURES location/Qualifiers
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/organism="unknown"
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LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066308
VERSION BD066308.1 GI:22611911
KEYWORDS JP 2001511000-A/943.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 943 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MEH
OS Unknown
PN JP 2001511000-A/943
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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